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NEWS 3 JAN 27 Source of Registration (SR) information in REGISTRY updated and searchable
NEWS 4 JAN 27 A new search aid, the Company Name Thesaurus, available in CA/CAplus
NEWS 5 FEB 05 German (DE) application and patent publication number format changes
NEWS 6 MAR 03 MEDLINE and LMEDLINE reloaded
NEWS 7 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 8 MAR 03 FRANCEPAT now available on STN
NEWS 9 MAR 29 Pharmaceutical Substances (PS) now available on STN
NEWS 10 MAR 29 WPIFV now available on STN
NEWS 11 MAR 29 No connect hour charges in WPIFV until May 1, 2004
NEWS 12 MAR 29 New monthly current-awareness alert (SDI) frequency in RAPRA
NEWS 13 APR 26 PROMT: New display field available
NEWS 14 APR 26 IFIPAT/IFIUDB/IFICDB: New super search and display field available
NEWS 15 APR 26 LITALERT now available on STN
NEWS 16 APR 27 NLDB: New search and display fields available

NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004

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FILE 'HOME' ENTERED AT 14:17:20 ON 29 APR 2004

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FILE 'JICST-EPLUS' ENTERED AT 14:18:46 ON 29 APR 2004
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=> s myelogenous leukemia
L1 22800 MYELOGENOUS LEUKEMIA

=> s myeloid cell proliferation
L2 142 MYELOID CELL PROLIFERATION

=> s "HOIPS I"
L3 18 "HOIPS I"

=> s l3 and l2
L4 0 L3 AND L2

=> s l3 and l1
L5 2 L3 AND L1

=> d 15 ti abs ibib tot

L5 ANSWER 1 OF 2 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:221411 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, UNITED STATES
 Ruben, Steven M., Olney, MD, UNITED STATES
PATENT ASSIGNEE(S): Human Genome Sciences, Inc. (U.S. corporation)

| | NUMBER | KIND | DATE |
|-----------------------|---------------------------------------------------------------------|------|--------------|
| PATENT INFORMATION: | US 2002119552 | A1 | 20020829 |
| APPLICATION INFO.: | US 2001-899917 | A1 | 20010709 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1997-994962, filed on 19 Dec 1997, PATENTED | | |

| | NUMBER | DATE |
|-----------------------|----------------|---------------|
| PRIORITY INFORMATION: | US 1996-33869P | 19961220 (60) |
| | US 1997-37388P | 19970207 (60) |
| DOCUMENT TYPE: | Utility | |

FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC, 20005-3934
NUMBER OF CLAIMS: 16
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 2059
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 2 OF 2 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2001:147697 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, United States
Ruben, Steven M., Olney, MD, United States
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)

| | NUMBER | KIND | DATE |
|-----------------------|-------------------------------------------|------|--------------|
| PATENT INFORMATION: | US 6284486 | B1 | 20010904 |
| APPLICATION INFO.: | US 1997-994962 | | 19971219 (8) |
| DOCUMENT TYPE: | Utility | | |
| FILE SEGMENT: | GRANTED | | |
| PRIMARY EXAMINER: | Carlson, Karen Cochranne | | |
| LEGAL REPRESENTATIVE: | Sterne, Kessler, Goldstein & Fox P.L.L.C. | | |
| NUMBER OF CLAIMS: | 69 | | |
| EXEMPLARY CLAIM: | 1 | | |
| NUMBER OF DRAWINGS: | 4 Drawing Figure(s); 4 Drawing Page(s) | | |
| LINE COUNT: | 1994 | | |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d his

(FILE 'HOME' ENTERED AT 14:17:20 ON 29 APR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, JICST-EPLUS' ENTERED AT 14:18:46 ON 29 APR 2004
L1 22800 S MYELOGENOUS LEUKEMIA
L2 142 S MYELOID CELL PROLIFERATION
L3 18 S "HOIPS I"
L4 0 S L3 AND L2
L5 2 S L3 AND L1

=> d l3 ti abs ibib tot

L3 ANSWER 1 OF 18 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I

polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:221411 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, UNITED STATES
Ruben, Steven M., Olney, MD, UNITED STATES
PATENT ASSIGNEE(S): Human Genome Sciences, Inc. (U.S. corporation)

| | NUMBER | KIND | DATE |
|-----------------------|---------------------------------------------------------------------|------|--------------|
| PATENT INFORMATION: | US 2002119552 | A1 | 20020829 |
| APPLICATION INFO.: | US 2001-899917 | A1 | 20010709 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1997-994962, filed on 19 Dec 1997, PATENTED | | |

| | NUMBER | DATE |
|-----------------------|--------------------------------------------------------------------------------------------------------------|---------------|
| PRIORITY INFORMATION: | US 1996-33869P | 19961220 (60) |
| | US 1997-37388P | 19970207 (60) |
| DOCUMENT TYPE: | Utility | |
| FILE SEGMENT: | APPLICATION | |
| LEGAL REPRESENTATIVE: | STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC, 20005-3934 | |
| NUMBER OF CLAIMS: | 16 | |
| EXEMPLARY CLAIM: | 1 | |
| NUMBER OF DRAWINGS: | 4 Drawing Page(s) | |
| LINE COUNT: | 2059 | |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 18 USPATFULL on STN
TI Human oncogene induced secreted protein I
AB The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2001:147697 USPATFULL
TITLE: Human oncogene induced secreted protein I
INVENTOR(S): Olsen, Henrik S., Gaithersburg, MD, United States
Ruben, Steven M., Olney, MD, United States
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)

| | NUMBER | KIND | DATE |
|-----------------------|-------------------------------------------|------|--------------|
| PATENT INFORMATION: | US 6284486 | B1 | 20010904 |
| APPLICATION INFO.: | US 1997-994962 | | 19971219 (8) |
| DOCUMENT TYPE: | Utility | | |
| FILE SEGMENT: | GRANTED | | |
| PRIMARY EXAMINER: | Carlson, Karen Cochran | | |
| LEGAL REPRESENTATIVE: | Sterne, Kessler, Goldstein & Fox P.L.L.C. | | |
| NUMBER OF CLAIMS: | 69 | | |
| EXEMPLARY CLAIM: | 1 | | |
| NUMBER OF DRAWINGS: | 4 Drawing Figure(s); 4 Drawing Page(s) | | |

LINE COUNT: 1994
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAW69220 Protein DGENE
AB This sequence is the human oncogene induced secreted protein I (HOIPS I) of the invention. HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.
ACCESSION NUMBER: AAW69220 Protein DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
CROSS REFERENCES: N-PSDB: AAV44745
DESCRIPTION: Human oncogene induced secreted protein I.

L3 ANSWER 4 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44751 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.
ACCESSION NUMBER: AAV44751 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N)HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag C02431.

L3 ANSWER 5 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44750 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (**HOIPS I**). **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44750 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T84854.

L3 ANSWER 6 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44749 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (**HOIPS I**). **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44749 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T92475.

L3 ANSWER 7 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44748 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (**HOIPS I**). **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute

and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44748 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag T91708.

L3 ANSWER 8 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44758 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44758 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 9 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44757 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44757 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 10 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44756 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.
ACCESSION NUMBER: AAV44756 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 11 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44755 DNA DGENE
AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.
ACCESSION NUMBER: AAV44755 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 12 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44754 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44754 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 13 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44753 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44753 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 14 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44752 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (**HOIPS I**) of the invention.
HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44752 DNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 15 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44746 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (**HOIPS I**). **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44746 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag.

L3 ANSWER 16 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44747 cDNA DGENE
AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (**HOIPS I**). **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44747 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.
PATENT INFO: WO 9828421 A1 19980702
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
DESCRIPTION: Expressed sequence tag AA340310.

L3 ANSWER 17 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia
AN AAV44745 cDNA DGENE
AB This sequence encodes the human oncogene induced secreted protein I (**HOIPS I**) of the invention. **HOIPS I** can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44745 cDNA DGENE
TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

INVENTOR: Olsen H S; Ruben S M
PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p
APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207
US 1996-33869 19961220

DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]
CROSS REFERENCES: P-PSDB: AAW69220
DESCRIPTION: Human oncogene induced secreted protein I coding sequence.

L3 ANSWER 18 OF 18 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia.
AN 1998-377652 [32] WPIDS
AB WO 9828421 A UPAB: 19980812
An isolated nucleic acid molecule (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to a sequence selected from:
(a) a NS encoding a polypeptide comprising amino acids from -20 to 142, -19 to 142, or 1 to 142 of the 162 amino acid (aa) sequence given in the specification (sequence representing a Human Oncogene Induced Secreted Protein I (**HOIPS I**) polypeptide);
(b) a NS encoding a polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825;
(c) a NS encoding a mature **HOIPS I** polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and
(d) a NS complementary to any of the NSs in (a)-(c).
Also claimed are:
(1) an isolated Nucleic Acid Molecule (NAM) comprising a PN which hybridises under stringent hybridisation conditions (I) where the PN which hybridises does not hybridise under stringent hybridisation conditions to a PN having a NS consisting of only A residues or of only T residues;
(2) an isolated NAM comprising a PN which encodes an amino acid sequence of an epitope-bearing portion of a **HOIPS I**

polypeptide having an amino acid sequence as in (a)-(c) above;

(3) an isolated NAM comprising a PN having a sequence at least 95% identical to a sequence selected from:

- (a) a NS of a fragment of a 860 bp sequence given in the specification (encoding the **HOIPS I** polypeptide), where the fragment comprises at least 50 contiguous nucleotides of the 860 bp, provided that the NS is not one of the 514, 457, 413, 320, 264, and 249 sequences given in the specification; and
- (b) a NS complementary to a NS as in (a);
- (4) a method for making a recombinant vector comprising inserting (I) into a vector;
- (5) a recombinant vector produced by a method as in (4);
- (6) a method of making a recombinant host cell comprising introducing a recombinant vector as in (5) into a host cell;
- (7) a recombinant host cell produced by a method as in (6);
- (8) an isolated **HOIPS I** polypeptide having an amino acid sequence at least 95% identical to a sequence encoded by (I) or an epitope-bearing portion of the polypeptide;
- (9) an isolated polypeptide comprising an epitope-bearing portion of the **HOIPS I** protein, where the portion is selected from a polypeptide comprising amino acid residues from -4 to 9, from 13 to 19, from 23 to 32, from 36 to 47, from 54 to 63, from 70 to 74, from 90 to 100, from 105 to 119 or from 125 to 132 of the 162 aa sequence;
- (10) an isolated **HOIPS I** polypeptide where, except for 1 to 50 conservative amino acid substitutions, the polypeptide has a sequence selected from:
 - (a) amino acids from -20 to 142, 19 to 142, or 1 to 142 of the 162 aa sequence given in the specification;
 - (b) an amino acid sequence of the **HOIPS I** polypeptide having an amino acid sequence encoded by a cDNA contained in ATCC 97825;
 - (c) an amino acid sequence of a mature **HOIPS I** polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and
 - (d) an amino acid sequence of an epitope-bearing portion of any one of the polypeptides as in (a)-(c);
- (11) an isolated nucleic acid encoding a polypeptide as in (10).

USE - The products can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis.

Dwg.0/3

ACCESSION NUMBER: 1998-377652 [32] WPIDS
 DOC. NO. NON-CPI: N1998-295209
 DOC. NO. CPI: C1998-114764
 TITLE: New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia.
 DERWENT CLASS: B04 D16 S03
 INVENTOR(S): OLSEN, H S; RUBEN, S M
 PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC
 COUNTRY COUNT: 81
 PATENT INFORMATION:

| PATENT NO | KIND DATE | WEEK | LA | PG |
|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|----|----|
| WO 9828421 | A1 19980702 (199832)* EN | 71 | | |
| RW: | AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW | | | |
| W: | AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW | | | |
| AU 9858027 | A 19980717 (199848) | | | |

US 6284486 B1 20010904 (200154)
US 2002119552 A1 20020829 (200259)

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|-----------------------------------------|----------------------------------------------------------------------|----------------------------------------------|
| WO 9828421 | A1 | WO 1997-US23547 | 19971219 |
| AU 9858027 | A | AU 1998-58027 | 19971219 |
| US 6284486 | B1 Provisional
Provisional | US 1996-33869P
US 1997-37388P
US 1997-994962 | 19961220
19970207
19971219 |
| US 2002119552 | A1 Provisional
Provisional
Div ex | US 1996-33869P
US 1997-37388P
US 1997-994962
US 2001-899917 | 19961220
19970207
19971219
20010709 |

FILING DETAILS:

| PATENT NO | KIND | PATENT NO |
|------------|------------|------------|
| AU 9858027 | A Based on | WO 9828421 |

PRIORITY APPLN. INFO: US 1997-37388P 19970207; US
1996-33869P 19961220; US
1997-994962 19971219; US
2001-899917 20010709

Refine Search

Search Results -

| Terms | Documents |
|------------|-----------|
| L9 and L10 | 18 |

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L11

Search History

DATE: Thursday, April 29, 2004 [Printable Copy](#) [Create Case](#)

Set Name Query
side by side

DB=USPT; PLUR=YES; OP=OR

| Set Name | Query | Hit Count | Set Name |
|----------|-------------------------------------------|-----------|----------------------------|
| L11 | l9 and L10 | 18 | <u>L11</u> |
| L10 | ruben.in. | 1520 | <u>L10</u> |
| L9 | l6 and L8 | 31 | <u>L9</u> |
| L8 | olsen.in. | 2539 | <u>L8</u> |
| L7 | henrik-olsen.in. | 0 | <u>L7</u> |
| L6 | myelogenous leukemia and L5 | 10350 | <u>L6</u> |
| L5 | myeloid proliferation and l4 | 29144 | <u>L5</u> |
| L4 | L3 and protein sequence | 614907 | <u>L4</u> |
| L3 | human oncogene induced secreted protein I | 1403401 | <u>L3</u> |
| L2 | HOIPs-I | 0 | <u>L2</u> |
| L1 | 6284486.pn. | 1 | <u>L1</u> |

END OF SEARCH HISTORY

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| Clear | Generate Collection | Print | Fwd Refs | Bkwd Refs |
| Generate OACS | | | | |

Search Results - Record(s) 1 through 10 of 18 returned.

1. Document ID: US 6632920 B1

L11: Entry 1 of 18

File: USPT

Oct 14, 2003

US-PAT-NO: 6632920

DOCUMENT-IDENTIFIER: US 6632920 B1

TITLE: 36 human secreted proteins

DATE-ISSUED: October 14, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|--------------------|--------------|-------|----------|---------|
| Olsen; Henrik S. | Gaithersburg | MD | | |
| Ruben; Steven M. | Olney | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Duan; Roxanne | Bethesda | MD | | |
| Florence; Kimberly | Rockville | MD | | |

US-CL-CURRENT: 530/300; 435/69.1, 530/324

| | | | | | | | | | | | | |
|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|-----------------------------|------------------------|----------------------|--------------------------|
| Full | Title | Citation | Front | Review | Classification | Date | Reference | Assignees | Attachments | Claims | KOMC | Drawn De |
|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|-----------------------------|------------------------|----------------------|--------------------------|

2. Document ID: US 6627741 B2

L11: Entry 2 of 18

File: USPT

Sep 30, 2003

US-PAT-NO: 6627741

DOCUMENT-IDENTIFIER: US 6627741 B2

TITLE: Antibodies to secreted protein HCEJQ69

DATE-ISSUED: September 30, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|------------------|------------|-------|----------|---------|
| Ruben; Steven M. | Olney | MD | | |
| Ni; Jian | Germantown | MD | | |

| | | |
|----------------------|---------------|----|
| Rosen; Craig A. | Laytonsville | MD |
| Wei; Ying-Fei | Berkeley | CA |
| Young; Paul | Gaithersburg | MD |
| Florence; Kimberly | Rockville | MD |
| Soppet; Daniel R. | Centreville | VA |
| Brewer; Laurie A. | St. Paul | MN |
| Endress; Gregory A. | Florence | MA |
| Carter; Kenneth C. | North Potomac | MD |
| Mucenski; Michael | Cincinnati | OH |
| Ebner; Reinhard | Gaithersburg | MD |
| LaFleur; David W. | Washington | DC |
| <u>Olsen; Henrik</u> | Gaithersburg | MD |
| Shi; Yanggu | Gaithersburg | MD |
| Moore; Paul A. | Germantown | MD |
| Komatsoulis; George | Silver Spring | MD |

US-CL-CURRENT: 530/389.2; 530/387.1, 530/387.3, 530/387.7, 530/387.9, 530/388.1,
530/388.15, 530/389.1

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequence](#) | [Attachments](#) | [Claims](#) | [KOMC](#) | [Drawn De](#)

3. Document ID: US 6605592 B2

L11: Entry 3 of 18

File: USPT

Aug 12, 2003

US-PAT-NO: 6605592

DOCUMENT-IDENTIFIER: US 6605592 B2

TITLE: Protein HOFNF53

DATE-ISSUED: August 12, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|---------------|-------|----------|---------|
| Ni; Jian | Germantown | MD | | |
| Baker; Kevin P. | Darnestown | MD | | |
| Birse; Charles E. | North Potomac | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Fiscella; Michele | Bethesda | MD | | |
| Komatsoulis; George A. | Silver Spring | MD | | |
| LaFleur; David W. | Washington | DC | | |
| Moore; Paul A. | Germantown | MD | | |
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |
| Soppet; Daniel R. | Centreville | VA | | |
| Young; Paul E. | Gaithersburg | MD | | |
| Wei; Ping | Brookeville | MD | | |

Florence; Kimberly A. Rockville MD

US-CL-CURRENT: 514/2; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/471, 435/69.1,
435/71.1, 435/71.2, 514/12, 514/8, 530/350

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Searches](#) | [Attachments](#) | [Claims](#) | [KINIC](#) | [Drawn Des](#)

4. Document ID: US 6590075 B2

L11: Entry 4 of 18

File: USPT

Jul 8, 2003

US-PAT-NO: 6590075

DOCUMENT-IDENTIFIER: US 6590075 B2

TITLE: Secreted protein HODAZ50

DATE-ISSUED: July 8, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-----------------------|---------------|-------|----------|---------|
| Ruben; Steven M. | Olney | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Fischer; Carrie L. | Burke | VA | | |
| Soppet; Daniel R. | Centreville | VA | | |
| Carter; Kenneth C. | North Potomac | MD | | |
| Bednarik; Daniel P. | Columbia | MD | | |
| Endress; Gregory A. | Potomac | MD | | |
| Yu; Guo-Liang | Berkeley | CA | | |
| Ni; Jian | Rockville | MD | | |
| Feng; Ping | Gaithersburg | MD | | |
| Young; Paul E. | Gaithersburg | MD | | |
| Greene; John M. | Gaithersburg | MD | | |
| Ferrie; Ann M. | Tewksbury | MA | | |
| Duan; Roxanne | Bethesda | MD | | |
| Hu; Jing-Shan | Sunnyvale | CA | | |
| Florence; Kimberly A. | Rockville | MD | | |
| Olsen; Henrik S. | Gaithersburg | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Shi; Yanggu | Gaithersburg | MD | | |

US-CL-CURRENT: 530/350; 435/6, 435/69.1, 435/7.1, 536/23.1

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Searches](#) | [Attachments](#) | [Claims](#) | [KINIC](#) | [Drawn Des](#)

5. Document ID: US 6576445 B1

L11: Entry 5 of 18

File: USPT

Jun 10, 2003

h e b b g e e e f e ef b e

US-PAT-NO: 6576445
 DOCUMENT-IDENTIFIER: US 6576445 B1

TITLE: Chemokine .alpha.-4

DATE-ISSUED: June 10, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|--------------|-------|----------|---------|
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |
| <u>Zeng; Zhi-Zhen</u> | Gaithersburg | MD | | |

US-CL-CURRENT: 435/69.5; 435/325, 530/300, 530/350, 530/386, 530/387.1, 530/387.3,
530/387.9, 530/388.1, 530/388.15, 530/388.23, 530/389.1, 530/389.2, 530/391.1,
530/391.3, 530/391.5, 530/391.7, 530/391.9

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn D](#)

6. Document ID: US 6566325 B2

L11: Entry 6 of 18

File: USPT

May 20, 2003

US-PAT-NO: 6566325
 DOCUMENT-IDENTIFIER: US 6566325 B2

TITLE: 49 human secreted proteins

DATE-ISSUED: May 20, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|---------------|-------|----------|---------|
| Moore; Paul A. | Germantown | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| Shi; Yanggu | Gaithersburg | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Florence; Kimberly A. | Rockville | MD | | |
| Soppet; Daniel R. | Centreville | VA | | |
| LaFleur; David W. | Washington | DC | | |
| Endress; Gregory A. | Potomac | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Komatsoulis; George | Silver Spring | MD | | |
| Duan; Roxanne D. | Bethesda | MD | | |

US-CL-CURRENT: 514/2; 530/300, 530/350

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn D](#)

7. Document ID: US 6548063 B1

L11: Entry 7 of 18

File: USPT

Apr 15, 2003

US-PAT-NO: 6548063

DOCUMENT-IDENTIFIER: US 6548063 B1

TITLE: Synferon

DATE-ISSUED: April 15, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|--------------------------|--------------|-------|----------|---------|
| <u>Olsen</u> ; Henrik S. | Gaithersburg | MD | | |
| Gentz; Reiner L. | Rockville | MD | | |
| <u>Ruben</u> ; Steven M. | Olney | MD | | |

US-CL-CURRENT: 424/158.1; 424/85.4, 435/325, 530/350, 530/351, 530/388.1, 530/389.1

| | | | | | | | | | | | | |
|------|-------|----------|-------|--------|----------------|------|-----------|----------|-------------|--------|-----|----------|
| Full | Title | Citation | Front | Review | Classification | Date | Reference | Examiner | Attachments | Claims | KMC | Drawn Ds |
|------|-------|----------|-------|--------|----------------|------|-----------|----------|-------------|--------|-----|----------|

 8. Document ID: US 6534631 B1

L11: Entry 8 of 18

File: USPT

Mar 18, 2003

US-PAT-NO: 6534631

DOCUMENT-IDENTIFIER: US 6534631 B1

TITLE: Secreted protein HT5GJ57

DATE-ISSUED: March 18, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|--------------------------|---------------|-------|----------|---------|
| <u>Ruben</u> ; Steven M. | Olney | MD | | |
| Komatsoulis; George | Silver Spring | MD | | |
| Duan; Roxanne D. | Bethesda | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Moore; Paul A. | Germantown | MD | | |
| Shi; Yanggu | Gaithersburg | MD | | |
| LaFleur; David W. | Washington | DC | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| <u>Olsen</u> ; Henrik | Gaithersburg | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Florence; Kimberly A. | Rockville | MD | | |
| Young; Paul | Gaithersburg | MD | | |
| Mucenski; Michael | Cincinnati | OH | | |
| Endress; Gregory A. | Potomac | MD | | |
| Soppet; Daniel R. | Centreville | VA | | |

US-CL-CURRENT: 530/350; 435/320.1, 435/325, 530/300, 536/23.1, 536/24.1

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|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|--------------------------|------------------------|---------------------|-----------------------|
| Full | Title | Citation | Front | Review | Classification | Date | Reference | Expedited | Attended | Claims | KMC | Drawn |
|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|--------------------------|------------------------|---------------------|-----------------------|

 9. Document ID: US 6525174 B1

L11: Entry 9 of 18

File: USPT

Feb 25, 2003

US-PAT-NO: 6525174

DOCUMENT-IDENTIFIER: US 6525174 B1

TITLE: Precerebellin-like protein

DATE-ISSUED: February 25, 2003

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|--------------------------|---------------|-------|----------|---------|
| Young; Paul | Gaithersburg | MD | | |
| Greene; John M. | Gaithersburg | MD | | |
| Ferrie; Ann M. | Tewksbury | MA | | |
| <u>Ruben</u> ; Steven M. | Olney | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Hu; Jing-Shan | Sunnyvale | CA | | |
| <u>Olsen</u> ; Henrik S. | Gaithersburg | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Moore; Paul A. | Germantown | MD | | |
| Shi; Yanggu | Gaithersburg | MD | | |
| Florence; Charles | Rockville | MD | | |
| Florence; Kimberly | Rockville | MD | | |
| Lafleur; David W. | Washington | DC | | |
| Ni; Jian | Rockville | MD | | |
| Fan; Ping | Gaithersburg | MD | | |
| Wei; Ying-Fei | Berkeley | CA | | |
| Fischer; Carrie L. | Burke | VA | | |
| Soppet; Daniel R. | Centreville | VA | | |
| Li; Yi | Sunnyvale | CA | | |
| Zeng; Zhizhen | Gaithersburg | MD | | |
| Kyaw; Hla | Frederick | MD | | |
| Yu; Guo-Liang | Berkeley | CA | | |
| Feng; Ping | Gaithersburg | MD | | |
| Dillon; Patrick J. | Carlsbad | CA | | |
| Endress; Gregory A. | Potomac | MD | | |
| Carter; Kenneth C. | North Potomac | MD | | |

US-CL-CURRENT: 530/350; 435/69.1

| | | | | | | | | | | | | |
|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|--------------------------|------------------------|---------------------|-----------------------|
| Full | Title | Citation | Front | Review | Classification | Date | Reference | Expedited | Attended | Claims | KMC | Drawn |
|----------------------|-----------------------|--------------------------|-----------------------|------------------------|--------------------------------|----------------------|---------------------------|---------------------------|--------------------------|------------------------|---------------------|-----------------------|

10. Document ID: US 6476195 B1

L11: Entry 10 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6476195

DOCUMENT-IDENTIFIER: US 6476195 B1

TITLE: Secreted protein HNFGF20

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|--------------------------|---------------|-------|----------|---------|
| Komatsoulis; George | Silver Spring | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| <u>Ruben</u> ; Steven M. | Olney | MD | | |
| Duan; Roxanne D. | Bethesda | MD | | |
| Moore; Paul A. | Germantown | MD | | |
| Shi; Yanggu | Gaithersburg | MD | | |
| LaFleur; David W. | Washington | DC | | |
| Wei; Ying-Fei | Berkeley | CA | | |
| Ni; Jian | Rockville | MD | | |
| Florence; Kimberly A. | Rockville | MD | | |
| Young; Paul | Gaithersburg | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Soppet; Daniel R. | Centreville | VA | | |
| Endress; Gregory A. | Potomac | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| <u>Olsen</u> ; Henrik | Gaithersburg | MD | | |
| Mucenski; Michael | Cincinnati | OH | | |

US-CL-CURRENT: 530/350; 435/6, 435/7.1, 536/23.1[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequence](#) | [Attachment](#) | [Claims](#) | [KOMC](#) | [Draw](#)[Clear](#) | [Generate Collection](#) | [Print](#) | [Fwd Refs](#) | [Bkwd Refs](#) | [Generate OACS](#)

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| L9 and L10 | 18 |

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11. Document ID: US 6475753 B1

L11: Entry 11 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6475753

DOCUMENT-IDENTIFIER: US 6475753 B1

TITLE: 94 Human Secreted Proteins

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|---------------------|---------------|-------|----------|---------|
| Ruben; Steven M. | Olney | MD | | |
| Ni; Jian | Rockville | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Wei; Ying-Fei | Berkeley | CA | | |
| Young; Paul | Gaithersburg | MD | | |
| Florence; Kimberly | Rockville | MD | | |
| Soppet; Daniel R. | Centreville | VA | | |
| Brewer; Laurie A. | St. Paul | MN | | |
| Endress; Gregory A. | Potomac | MD | | |
| Carter; Kenneth C. | Potomac | MD | | |
| Mucenski; Michael | Cincinnati | OH | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Lafleur; David W. | Washington | DC | | |
| Olsen; Henrik | Gaithersburg | MD | | |
| Shi; Yanggu | Gaithersburg | MD | | |
| Moore; Paul A. | Germantown | MD | | |
| Komatsoulis; George | Silver Spring | MD | | |

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/325, 435/471, 435/69.4,
435/71.1, 530/350, 536/23.5[Full](#) [Title](#) [Citation](#) [Front](#) [Review](#) [Classification](#) [Date](#) [Reference](#) [Description](#) [Abstract](#) [Claims](#) [KUDC](#) [Drawn D](#)

12. Document ID: US 6433139 B1

L11: Entry 12 of 18

File: USPT

Aug 13, 2002

US-PAT-NO: 6433139

DOCUMENT-IDENTIFIER: US 6433139 B1

TITLE: Secreted protein HPEAD48

DATE-ISSUED: August 13, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|------------------|--------------|-------|----------|---------|
| Ruben; Steven M. | Olney | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Olsen; Henrik S. | Gaithersburg | MD | | |

US-CL-CURRENT: 530/350; 435/6, 435/7.1, 530/300, 536/23.1[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequence](#) | [Attachment](#) | [Claims](#) | [KIMC](#) | [Draw. De](#) 13. Document ID: US 6420526 B1

L11: Entry 13 of 18

File: USPT

Jul 16, 2002

US-PAT-NO: 6420526

DOCUMENT-IDENTIFIER: US 6420526 B1

TITLE: 186 human secreted proteins

DATE-ISSUED: July 16, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-----------------------|---------------|-------|----------|---------|
| Ruben; Steven M. | Olney | MD | | |
| Rosen; Craig A. | Laytonsville | MD | | |
| Fischer; Carrie L. | Burke | VA | | |
| Soppet; Daniel P. | Centreville | VA | | |
| Carter; Kenneth C. | North Potomac | MD | | |
| Bednarik; Daniel R. | Columbia | MD | | |
| Endress; Gregory A. | Potomac | MD | | |
| Yu; Guo-Liang | Berkeley | CA | | |
| Ni; Jian | Rockville | MD | | |
| Feng; Ping | Gaithersburg | MD | | |
| Young; Paul E. | Gaithersburg | MD | | |
| Greene; John M. | Gaithersburg | MD | | |
| Ferrie; Ann M. | Tewksbury | MA | | |
| Duan; Roxanne | Bethesda | MD | | |
| Hu; Jing-Shan | Sunnyvale | CA | | |
| Florence; Kimberly A. | Rockville | MD | | |
| Olsen; Henrik S. | Gaithersburg | MD | | |
| Ebner; Reinhard | Gaithersburg | MD | | |
| Brewer; Laurie A. | St. Paul | MN | | |

| | | |
|-------------------|--------------|----|
| Moore; Paul A. | Germantown | MD |
| Shi; Yanggu | Gaithersburg | MD |
| Lafleur; David W. | Washington | DC |
| Li; Yi | Sunnyvale | CA |
| Zeng; Zhizhen | Lansdale | PA |
| Kyaw; Hla | Frederick | MD |

US-CL-CURRENT: 530/350; 435/6, 536/23.1

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequencies](#) | [Attachments](#) | [Claims](#) | [KOMC](#) | [Draw. De](#)

14. Document ID: US 6379926 B1

L11: Entry 14 of 18

File: USPT

Apr 30, 2002

US-PAT-NO: 6379926

DOCUMENT-IDENTIFIER: US 6379926 B1

TITLE: Polynucleotides encoding chemokine .beta.-6 antagonists

DATE-ISSUED: April 30, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------|--------------|-------|----------|---------|
| Kreider; Brent L. | Germantown | MD | | |
| Ruben; Steven M. | Olney | MD | | |
| Olsen; Henrik S. | Gaithersburg | MD | | |

US-CL-CURRENT: 435/69.5; 435/252.3, 435/320.1, 435/325, 435/455, 435/471, 435/69.1,
435/69.7, 536/23.1, 536/23.4, 536/23.5

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequencies](#) | [Attachments](#) | [Claims](#) | [KOMC](#) | [Draw. De](#)

15. Document ID: US 6342581 B1

L11: Entry 15 of 18

File: USPT

Jan 29, 2002

US-PAT-NO: 6342581

DOCUMENT-IDENTIFIER: US 6342581 B1

** See image for Certificate of Correction **

TITLE: Secreted protein HLHFP03

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|------------------|--------------|-------|----------|---------|
| Rosen; Craig A. | Laytonsville | MD | | |
| Ruben; Steven M. | Olney | MD | | |

Olsen; Henrik S. Gaithersburg MD
Ebner; Reinhard Gaithersburg MD

US-CL-CURRENT: 530/300; 435/69.1, 530/350

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Dependencies](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn D](#)

16. Document ID: US 6284486 B1

L11: Entry 16 of 18 File: USPT Sep 4, 2001

US-PAT-NO: 6284486

DOCUMENT-IDENTIFIER: US 6284486 B1

TITLE: Human oncogene induced secreted protein I

DATE-ISSUED: September 4, 2001

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|--------------|-------|----------|---------|
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |

US-CL-CURRENT: 435/69.1; 435/252.3, 435/6, 435/91.1, 435/91.4, 435/91.41, 536/23.1,
536/23.5, 536/24.1, 536/24.2

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Dependencies](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn D](#)

17. Document ID: US 6114145 A

L11: Entry 17 of 18 File: USPT Sep 5, 2000

US-PAT-NO: 6114145

DOCUMENT-IDENTIFIER: US 6114145 A

TITLE: Synferon, a synthetic interferon

DATE-ISSUED: September 5, 2000

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|--------------|-------|----------|---------|
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| <u>Gentz; Reiner L.</u> | Rockville | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |

US-CL-CURRENT: 435/69.51; 424/85.4, 435/252.3, 435/252.33, 435/254.11, 435/325,
435/455, 435/471, 435/91.41, 530/351, 536/23.52

[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Dependencies](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn D](#)

18. Document ID: US 5916769 A

L11: Entry 18 of 18

File: USPT

Jun 29, 1999

US-PAT-NO: 5916769

DOCUMENT-IDENTIFIER: US 5916769 A

TITLE: Polynucleotides encoding extra cellular/epidermal growth factor HCABA58X polypeptides

DATE-ISSUED: June 29, 1999

INVENTOR-INFORMATION:

| NAME | CITY | STATE | ZIP CODE | COUNTRY |
|-------------------------|--------------|-------|----------|---------|
| <u>Olsen; Henrik S.</u> | Gaithersburg | MD | | |
| <u>Ruben; Steven M.</u> | Olney | MD | | |

US-CL-CURRENT: 435/69.4; 435/243, 435/320.1, 435/325, 435/69.1, 536/23.1, 536/23.51[Full](#) | [Title](#) | [Citation](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Searchable](#) | [Attachments](#) | [Claims](#) | [KIMC](#) | [Drawn De](#)[Clear](#) | [Generate Collection](#) | [Print](#) | [Fwd Refs](#) | [Bkwd Refs](#) | [Generate OACS](#)

| | |
|------------|-----------|
| Terms | Documents |
| L9 and L10 | 18 |

Display Format: [CIT](#) | [Change Format](#)[Previous Page](#) [Next Page](#) [Go to Doc#](#)

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OM protein - protein search, using sw model
Run on: April 29, 2004, 15:21:06 : Search time 58 seconds
(w/o alignments)
789,184 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862

Sequence: I MKGFTATIFLWTIIFPSGSG.....ELYTERKSTVACANATIMCS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Maximum Match 10%
Listing first 45 summaries

Database : A_GeneseqP_29Jan04:
1: geneseqP1980s:
2: geneseqP1990s:
3: geneseqP2000s:
4: geneseqP2001s:
5: geneseqP2002s:
6: geneseqP2003s:
7: geneseqP2003bs:
8: geneseqP2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query #

No. Match Length DB ID Description

| | | | | | | |
|----|-------|-------|-----|---|----------|----------------------------------------------------------------------------|
| 1 | 862 | 100.0 | 162 | 2 | AAW69220 | Raw69220 Human onc gene induced secreted protein I. |
| 2 | 862 | 100.0 | 162 | 2 | AK13933 | Raw13933 Human onc gene induced secreted protein I. |
| 3 | 862 | 100.0 | 162 | 7 | AD59274 | Raw59274 Human onc gene induced secreted protein I. |
| 4 | 854 | 99.1 | 162 | 3 | AY77476 | Raw77476 Human onc gene induced secreted protein I. |
| 5 | 850 | 98.6 | 162 | 6 | ABU1841 | Raw61841 Human onc gene induced secreted protein I. |
| 6 | 758 | 87.9 | 162 | 3 | AAW84000 | Raw84000 Human onc gene induced secreted protein I. |
| 7 | 613 | 71.1 | 162 | 2 | AY13932 | Raw13932 Human onc gene induced secreted protein I. |
| 8 | 613 | 71.1 | 162 | 3 | AY77481 | Raw77481 Human onc gene induced secreted protein I. |
| 9 | 613 | 71.1 | 162 | 6 | ABU1846 | Raw61846 Rodent onc gene induced secreted protein I. |
| 10 | 613 | 71.1 | 162 | 7 | AD59272 | Raw59272 Rat onc gene induced secreted protein I. |
| 11 | 336 | 39.0 | 160 | 6 | ABU1847 | Raw61847 Chicken onc gene induced secreted protein I. |
| 12 | 336 | 39.0 | 160 | 2 | AY13929 | Raw13929 Murine onc gene induced secreted protein I. |
| 13 | 106 | 12.3 | 160 | 3 | AD5928 | Raw5928 Murine onc gene induced secreted protein I. |
| 14 | 106 | 12.3 | 160 | 2 | AY13931 | Raw13931 Human onc gene induced secreted protein I. |
| 15 | 101.5 | 11.8 | 160 | 2 | AD5927 | Raw5927 Human onc gene induced secreted protein I. |
| 16 | 101.5 | 11.8 | 160 | 3 | AY77478 | Raw77478 Avian onc gene induced secreted protein I. |
| 17 | 101.5 | 11.8 | 160 | 6 | ABU1843 | Raw61843 Updated human onc gene induced secreted protein I. |
| 18 | 96.5 | 11.2 | 141 | 3 | AY77480 | Raw77480 Primate onc gene induced secreted protein I. |
| 19 | 96.5 | 11.2 | 141 | 3 | ABU1845 | Raw61845 Mouse onc gene induced secreted protein I. |
| 20 | 96.5 | 9.2 | 484 | 5 | ABR91964 | Raw91964 Herbicide resistance protein onc gene induced secreted protein I. |
| 21 | 78 | 9.0 | 876 | 6 | ABU91940 | Raw91940 Protein onc gene induced secreted protein I. |
| 22 | 77 | 8.9 | 363 | 3 | AAG28947 | Raw28947 Arabidopsis onc gene induced secreted protein I. |
| 23 | 77 | 8.9 | 354 | 3 | AAG28946 | Raw28946 Arabidopsis onc gene induced secreted protein I. |
| 24 | 77 | 8.9 | 177 | 6 | ABU17986 | Raw17986 Protein onc gene induced secreted protein I. |

ALIGNMENTS

| | | | | | | |
|----|------|-----|------|---|----------|----------------------------------------------------------------------------|
| 26 | 75.5 | 8.8 | 342 | 6 | ABU26566 | Raw26566 Protein onc gene induced secreted protein I. |
| 28 | 75.5 | 8.8 | 1207 | 3 | AAG30768 | Raw30768 Arabidopsis onc gene induced secreted protein I. |
| 29 | 75.5 | 8.8 | 1215 | 3 | AAG30766 | Raw30766 Arabidopsis onc gene induced secreted protein I. |
| 30 | 75.5 | 8.8 | 1241 | 6 | ABU24033 | Raw24033 Protein onc gene induced secreted protein I. |
| 31 | 75 | 8.7 | 377 | 2 | AAV23037 | Raw23037 Bovine onc gene induced secreted protein I. |
| 32 | 75 | 8.7 | 505 | 7 | ADB75603 | Raw75603 Prostate onc gene induced secreted protein I. |
| 33 | 75 | 8.7 | 524 | 3 | ABR56960 | Raw56960 Human onc gene induced secreted protein I. |
| 34 | 75 | 8.7 | 699 | 5 | ABB91291 | Raw91291 Herbicide resistance protein onc gene induced secreted protein I. |
| 35 | 75 | 8.7 | 392 | 2 | AYV2057 | Raw2057 Bovine onc gene induced secreted protein I. |
| 36 | 74 | 8.6 | 264 | 2 | ABR29640 | Raw29640 PCTD ORF onc gene induced secreted protein I. |
| 37 | 73.5 | 8.5 | 851 | 7 | ADC64335 | Raw64335 KIAA1956 onc gene induced secreted protein I. |
| 38 | 72.5 | 8.4 | 1172 | 5 | ABP23009 | Raw23009 Human polypeptide onc gene induced secreted protein I. |
| 39 | 72.5 | 8.4 | 1178 | 5 | ABP23008 | Raw23008 Human polypeptide onc gene induced secreted protein I. |
| 40 | 72.5 | 8.4 | 269 | 4 | ABP95041 | Raw95041 Human onc gene induced secreted protein I. |
| 41 | 72 | 8.4 | 608 | 5 | ABP5507 | Raw5507 Human onc gene induced secreted protein I. |
| 42 | 72 | 8.4 | 700 | 5 | ABP2360 | Raw2360 Herbicide resistance protein onc gene induced secreted protein I. |
| 43 | 72 | 8.4 | 790 | 5 | AAO19184 | Raw19184 Human neu onc gene induced secreted protein I. |
| 44 | 72 | 8.4 | 310 | 6 | ABM70549 | Raw70549 Photorhabdus onc gene induced secreted protein I. |

Abu26566 Protein onc gene induced secreted protein I.
Raw30768 Arabidopsis onc gene induced secreted protein I.
Raw30766 Arabidopsis onc gene induced secreted protein I.
Raw24033 Protein onc gene induced secreted protein I.
Raw23037 Bovine onc gene induced secreted protein I.
Raw75603 Prostate onc gene induced secreted protein I.
Raw56960 Human onc gene induced secreted protein I.
Raw91291 Herbicide resistance protein onc gene induced secreted protein I.
Raw2057 Bovine onc gene induced secreted protein I.
Raw29640 PCTD ORF onc gene induced secreted protein I.
Raw64335 KIAA1956 onc gene induced secreted protein I.
Raw23009 Human polypeptide onc gene induced secreted protein I.
Raw23008 Human polypeptide onc gene induced secreted protein I.
Raw95041 Human onc gene induced secreted protein I.
Raw5507 Human onc gene induced secreted protein I.
Raw2360 Herbicide resistance protein onc gene induced secreted protein I.
Raw19184 Human neu onc gene induced secreted protein I.
Raw70549 Photorhabdus onc gene induced secreted protein I.

Abu69220 standard; protein; 162 AA.

XX

AC

AAW69220;

XX

DT

16-OCT-1998

(first entry)

XX

DB

Human oncogene induced secreted protein I.

XX

KW

Oncogene induced secreted protein I; HOIPS I; human; cancer; therapy;

XX

KW

cell proliferative disease; myelogenous leukaemia;

XX

KW

cell differentiation disorder.

XX

OS

Homo sapiens.

XX

PH

Key

Location/Qualifiers

1..20

/Note= "signal peptide"

21..162

FT

Protein

FT

/note= "mature HOIPS I"

XX

PN

W09828421-A1.

XX

PD

02-JUL-1998.

XX

PP

19-DBC-1997;

97MO-US023547.

XX

PR

20-DBC-1996;

96US-00338699.

PR

07-FBB-1997;

97US-0037388P.

PR

07-FBB-1997;

97US-0037388P.

PR

N-PSDB; AAV44745.

XX

DR

WPI; 1998-377652/32.

WPI; 1998-377652/32.

N-PSDB; AAV44745.

XX

DR

N-PSDB; AAV44745.

XX

PR

Claim 12; Page 51-52; 71pp; English.

PR

CC

This sequence is the human oncogene induced secreted protein I (HOIPS I).

CC

of the invention. HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukemias. The products can also be used for detection and diagnosis of

CC

leukemias. The products can also be used for detection and diagnosis of

CC

| | | | |
|--------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|----------------------------------------------------------------|
| CC | a cell proliferative or cell differentiation disorders | Db | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 |
| XX | | Ov | 61 QLKSNNIRFGILRBDIEKLFLDLAMQSSVLFNSYSPICELALKPSFCGRRKGEQI 120 |
| SQ | Sequence 162 AA; | Db | 61 QLKSNNIRFGILRBDIEKLFLDLAMQSSVLFNSYSPICELALKPSFCGRRKGEQI 120 |
| | Query Match 100.0%; Score 862; DB 2; Length 162; | Ov | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| | Best Local Similarity 100.0%; Pred. No. 9e-92; Mismatches 0; Indels 0; Gaps 0; | Db | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | Ov | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 |
| QY | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 | Db | 61 QLKSNNIRFGILRBDIEKLFLDLAMQSSVLFNSYSPICELALKPSFCGRRKGEQI 120 |
| Db | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 | Ov | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| QY | 61 QLKSNNIRFGILRBDIEKLFLDLAMQSSVLFNSYSPICELALKPSFCGRRKGEQI 120 | Db | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| Db | 61 QLKSNNIRFGILRBDIEKLFLDLAMQSSVLFNSYSPICELALKPSFCGRRKGEQI 120 | Ov | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| QY | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 | Db | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| Db | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 | Ov | 121 YYAGPVNNPEFTIPOGEYQVILELYTEKSTVACANATMCS 162 |
| | | RESULT 2 | |
| | | AY13933 | |
| ID | AY13933 standard; protein; 162 AA. | Ov | |
| XX | | Db | |
| AC | AY13933; | Ov | |
| XX | | Db | |
| DT | 14-JUL-1999 (first entry) | Ov | |
| XX | | Db | |
| DE | Human OHP106 protein. | Ov | |
| XX | | Db | |
| KW | OHP106; bacterial; viral; infection; cytokine activity; tissue formation; cell proliferation; cell differentiation; immunostimulation; therapy; immunosuppression; haematopoiesis control; tissue repair. | Ov | |
| XX | | Db | |
| OS | Homo sapiens. | Ov | |
| XX | | Db | |
| PN | W0918205-A1. | Ov | |
| XX | | Db | |
| PD | 15-APR-1999. | Ov | |
| XX | | Db | |
| PP | 06-OCT-1998; 98WO-JP004515. | Ov | |
| XX | | Db | |
| PR | 07-OCT-1997; 97JP-00274673. | Ov | |
| XX | | Db | |
| PA | (ONO) ONO PHARM CO LTD. | Ov | |
| XX | | Db | |
| PD | WPI; 1998-277269/23, AAX36696. | Ov | |
| XX | | Db | |
| PT | New polypeptides useful in the treatment of various diseases including bacterial and viral infections with cytokine activity. | Ov | |
| XX | | Db | |
| PI | Honjo T, Kato K, Tada H; | Ov | |
| XX | | Db | |
| DR | WPI; 1998-277269/23, AAX36695, AAX36696. | Ov | |
| XX | | Db | |
| PT | Claim 1; Page 47; 57pp; Japanese. | Ov | |
| XX | | Db | |
| PR | This sequence represents a OHP106 protein of the invention. The polypeptides and their antibodies are applicable in drug compositions, useful for treatment of various diseases including bacterial and viral infections with cytokine activity, and activities e.g. on cell haemopoiesis, and tissue formation and repair. The proteins and antibodies have a wide spectrum of activities | Ov | |
| XX | | Db | |
| PT | Sequence 162 AA; | Ov | |
| XX | | Db | |
| PT | Query Match 100.0%; Score 862; DB 2; Length 162; | Ov | |
| Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | Db | |
| QY | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 | Ov | |
| | | RESULT 3 | |
| | | ADE59274 | |
| ID | ADE59274 standard; protein; 162 AA. | Ov | |
| XX | | Db | |
| AC | ADE59274; | Ov | |
| XX | | Db | |
| DT | 29-JAN-2004 (first entry) | Ov | |
| XX | | Db | |
| DE | Human Protein O95711, SEQ ID NO 5168. | Ov | |
| XX | | Db | |
| KW | Human; pain; neuronal tissue; gene therapy; CCI; spinal segmental nerve injury; chronic constriction injury; Chung; spared nerve injury; SNI; Chung. | Ov | |
| XX | | Db | |
| OS | Homo Sapiens. | Ov | |
| XX | | Db | |
| PF | WO2003016475-A2. | Ov | |
| XX | | Db | |
| PD | 27-FEB-2003. | Ov | |
| XX | | Db | |
| PR | 14-AUG-2002; 2002WO-US025765. | Ov | |
| XX | | Db | |
| PR | 14-AUG-2001; 2001US-0312147P. | Ov | |
| XX | | Db | |
| PR | 01-NOV-2001; 2001US-0346382P. | Ov | |
| XX | | Db | |
| PR | 26-NOV-2001; 2001US-0333347P. | Ov | |
| XX | | Db | |
| PA | (GEHO) GEN HOSPITAL CORP. | Ov | |
| XX | | Db | |
| PA | {PARB } BAYER AG. | Ov | |
| XX | | Db | |
| PT | Woolf C, D'urso D, Befort K, Costigan M; | Ov | |
| XX | | Db | |
| PR | WPI; 2003-268312/26. | Ov | |
| XX | | Db | |
| DR | GENBANK; 095711. | Ov | |
| XX | | Db | |
| PT | New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal. | Ov | |
| XX | | Db | |
| PT | Claim 1; Page; 1017pp; English. | Ov | |
| XX | | Db | |
| CC | The invention discloses a composition comprising two or more isolated rat or human poly nucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence or human poly nucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell expressing the vector, a method for identifying a nucleotide sequence expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of | Ov | |
| CC | Query Match 100.0%; Score 862; DB 2; Length 162; | Ov | |
| CC | Best Local Similarity 100.0%; Pred. No. 9e-92; Mismatches 0; Indels 0; Gaps 0; | Ov | |
| CC | Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Ov | |
| CC | 1 MKGFTATLFLWLTIFPSCSGGGKAWPHTWVCSDSGLAVLYQSCDPLQPGFSEVKCSK 60 | Ov | |

Sequence 162 AA;

Query Match 100.0%; Score 862; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 9e-92; Matches 162;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGFTATLFLWLTIFPSCSGGGAKKAMPTATHVCSDSLCEVLYOSCDIQLQDFRSVTKCSK 60
 1 MKGFTATLFLWLTIFPSCSGGGAKKAMPTATHVCSDSLCEVLYOSCDIQLQDFRSVTKCSK 60
 Db 61 QJKSNINRFGTIREDKIELFDLAIMSQGSVNLNISYPICHAALKFSFGRRKEQI 122
 61 QJKSNINRFGTIREDKIELFDLAIMSQGSVNLNISYPICHAALKFSFGRRKEQI 122
 QY 121 YYAGPVNNPEFTIPQGEVQVLILYTERKSTVACANATIMCS 162
 121 YYAGPVNNPEFTIPQGEVQVLILYTERKSTVACANATIMCS 162
 Db

RESULT 4

ID AAY77476 standard; protein; 162 AA.

XX

AC AAY77476;

XX

DT 05-JUN-2000 (first entry)

DE Human MD-1 protein.

XX

KW MD-1; MD-2; leucine-rich motif; IRR protein ligand; immune disorder; inflammatory; allergy; immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory; dermatological; antithyroid.

XX

OS Homo sapiens.

XX

PN WO200001817-A2.

XX

PD 13-JAN-2000.

XX

PP 06-JUL-1999; 99WO-US012366.

XX

PR 06-JUL-1999; 98US-00110938.

PR 13-JUL-1998; 98US-00114466.

PR 23-JUL-1998; 98US-0093897P.

PR 12-AUG-1998; 98US-00132968.

PR 18-AUG-1998; 98US-00136214.

PR 11-SEP-1998; 98US-0099999P.

XX

PA (SCHERING CORP.

PI Bates EBM, Lebecque SJE, Murphy EE, Martson JD, Gorman DM,
 PI Pedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA,
 PI Sazan JP, Mahony D, Lees EM;

XX

DR WPI; 2000-171015/15.

DR N/P SDB; AA224417.

PT New isolated mammalian genes, used to develop products for treating e.g.
 PT immune, inflammatory or allergic abnormalities, cancers or degenerative
 PT conditions.

XX

PS Claim 43; Page 203-204; 218pp; English.

CC The invention relates to a number of primate and/or rodent proteins and
 CC the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (Dc-PGTR); the TNF (tumour necrosis factor
 receptor family-related proteins HTDEB4, HSJUD7R and RANKL; human CC
 CC chemokine HCC5; human deubiquitinating Proteins Dub1 and Dub 12; human

MD-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proliferation, or differentiation of cells), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, or abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute and chronic inflammatory diseases in which T cell activation, expansion, and/or immunological T cell memory play an important role. Sequences AAY77476-Y77480 represent MD-1 and MD-2 proteins. AAY77476 is human MD-1, AAY77477-Y77478 are human MD-2 proteins, AAY77479 is murine MD-2 and AAY77480 is a primate MD-2.

XX DR WPI; 2003-466159/44.
 XX DR N-PSDB; ACH62461.
 PT New composition comprising HCC5', Dub1', Dub12', primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.
 XX PS Claim 1; Page 15-16; 77pp; English.
 CC The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of human MD1.
 XX SQ Sequence 162 AA:
 Query Match 98.6%; Score 850; DB 6; Length 162;
 Best Local Similarity 98.8%; Pred. No. 2; e-90; Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MKGETATIFLWTNIPFSSGGGGKAMPTHVCSDSLEVLYQSCDPLQDFGSVEKSK 60
 1 MKGETATIFLWTNIPFSSGGGGKAMPTHVCSDSLEVLYQSCDPLQDFGSVEKSK 60
 Db 61 QLKSNINIRFGTILREDIKEFLDIALMSQGSVNLNSYPICBALPKFSRGRKGQEI 120
 QY 61 QLKSNINIRFGTILREDIKEFLDIALMSQGSVNLNSYPICBALPKFSRGRKGQEI 120
 Db 121 YYAGPVNNRFPFTIPOGEYQVLLBLTYERGSTVACANITMCS 162
 QY 121 YYAGPVNNRFPFTIPOGEYQVLLBLTYERGSTVACANITMCS 162
 Db 121 YYAGPVNNRFPFTIPOGEYQVLLBLTYERGSTVACANITMCS 162
 RESULT 6
 AAY84000 ID AAY84000 standard; protein; 162 AA.
 AC AAY84000;
 XX DE Human B-cell surface protein MD-1.
 DT 25-OCT-2000 (first entry)
 DE Human B-cell surface protein MD-1.
 FH Human: B cell; surface protein; apoptosis; antiallergic; allergy; EST; KW antiasthmatic; immunosuppressive; dermatological; antiinflammatory; autoimmune disease; asthma; atopic dermatitis; expressed sequence tag.
 OS Homo sapiens.
 FT Key location/Qualifiers 1..19
 FT /note= "signal peptide"
 FT Protein 20..162
 FT /note= "mature MD-1 protein"
 PN JP2000106880-A.
 PD 18-APR-2000.
 XX PP 08-OCT-1998; 980P-00286470.
 PR 08-OCT-1998; 980P-00286470.
 PA (MITSUBISHI CHEM CORP.
 XX DR WPI; 2000-355476/31.
 DR N-PSDB; AAN11221.
 PT A new DNA encoding a human B cell surface protein, useful for treating autoimmune diseases, allergic diseases, asthma and atopic dermatitis.
 XX PS Claim 1; Page 11; 12pp; Japanese.

XX CC This sequence represents a human B cell surface protein, designated MD-1. The protein is involved in the inhibition or induction of B cell apoptosis and has anti-allergic, antiasthmatic, immunosuppressive, dermatological and anti-inflammatory activity. The protein and the DNA are used as treating and diagnostic agents for diseases related to antibody production by B cells, e.g. autoimmune or allergic diseases, asthma and atopic dermatitis. The coding sequence was isolated from a human EST clone (GenBank accession number T84054).
 XX SQ Sequence 162 AA:
 Query Match 87.9%; Score 758; DB 3; Length 162;
 Best Local Similarity 88.9%; Prod. No. 1; e-79; Matches 144; Conservative 3; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MKGETATIFLWTNIPFSSGGGGKAMPTHVCSDSLEVLYQSCDPLQDFGSVEKSK 60
 Db 1 MKGETATIFLWTNIPFSSGGGGKAMPTHVCSDSLEVLYQSCDPLQDFGSVEKSK 60
 QY 61 QLKSNINIRFGTILREDIKEFLDIALMSQGSVNLNSYPICBALPKFSRGRKGQEI 120
 Db 61 QLKSNINIRFGTILREDIKEFLDIALMSQGSVNLNSYPICBALPKFSRGRKGQEI 120
 QY 121 YYAGPVNNRFPFTIPOGEYQVLLBLTYERGSTVACANITMCS 162
 Db 121 YYAGPVNNRFPFTIPOGEYQVLLBLTYERGSTVACANITMCS 162
 RESULT 7
 AAY13932 ID AAY13932 standard; protein; 162 AA.
 AC AAY13932;
 XX DT 14-JUL-1999 (first entry)
 XX DE Mouse OHP106 protein.
 XX KW OHP106; bacterial; viral; infection; cytokine activity; tissue formation; KW cell proliferation; cell differentiation; immunostimulation; therapy;
 KW immunosuppression; haematopoiesis control; tissue repair.
 OS Mus musculus.
 XX PN WO9918205-A1.
 XX PD 15-APR-1999.
 XX PF 06-OCT-1998; 98W0-JP004515.
 PR 07-OCT-1997; 97JP-00274673.
 XX PA (ONO) ONO PHARM CO LTD.
 PI Honjo T, Kato K, Tada H;
 XX DR WPI; 1999-277269/23.
 DR N-PSDB; AAX36693, AAX36694.
 XX PT New polypeptides useful in the treatment of various diseases including bacterial and viral infections with cytokine activity.
 XX PS Claim 1; Page 44; 57pp; Japanese.
 XX CC This sequence represents a OHP106 protein of the invention. The polypeptides and their antibodies are applicable in drug compositions, useful for treatment of various diseases including bacterial and viral infections with cytokine activity, and activities e.g. on cell proliferation/differentiation, immunostimulation/suppression, control of hematopoiesis, and tissue formation and repair. The proteins and antibodies have a wide spectrum of activities.

| sq | Sequence 162 AA; | Query Match | 71.1%; Score 613; DB 2; | Length 162; |
|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|--------------------------------------------------------|--------------------------------------------------------------|
| Best Local Similarity | 66.7%; Pred. No. 8.5-63; | Mismatches | 32; | Indels 0; Gaps 0 |
| Matches | 108; Conservative 22; | MMatches | 32; | Indels 0; Gaps 0 |
| 1 | MKGFTATLFLMLTLLIFESCGGGKAWPPTWVCDGSLVYQSCPDQFGSVVERSK | Db | 1 | MNGVALALLWLWLTSSSDHGSENGWPKHTACNSGGLEVVYQSCDPDQFGSLSIDQSK 60 |
| QY | 61 QLKSNTNIRGILRDIKEFLDLMSGSVNFNSTPICEALPKFSPCFRRKQPI | Db | 61 QIQSNTNIRFGILRDIKEFLDLMSGSVNFNSTPICEALPKFSPCFRRKQPI | 120 |
| OY | 61 YYAGPVNNEPFITPOQFQYQVILBITEKRSVACANATIMCS 162 | Db | 121 YYAGPVNNEPFITPOQFQYQVILBITEKRSVACANATIMCS 162 | 120 |
| OY | 121 YYAGPVNNEPFITPOQFQYQVILBITEKRSVACANATIMCS 162 | Db | 121 YYAGPVNNEPFITPOQFQYQVILBITEKRSVACANATIMCS 162 | 120 |
| RESULT 8 | | | | |
| AAY77481 | | | | |
| ID | AAY77481 standard; protein: 162 AA. | | | |
| XX | | | | |
| AC | AAY77481; | | | |
| XX | | | | |
| DT | 05-JUN-2000 (first entry) | | | |
| XX | Rodent protein sequence, SEQ ID NO:50. | | | |
| XX | | | | |
| KM | Immune disorder; inflammation; allergy; immunosuppressant; antiarthritic; | | | |
| KW | antirheumatoid; antiinflammatory; dermatological; antithyroid. | | | |
| XX | | | | |
| OS | Rodentia. | | | |
| XX | | | | |
| PN | WO200001817-A2. | | | |
| XX | | | | |
| PD | 13-JAN-2000. | | | |
| XX | | | | |
| PF | 99WO-US012366. | | | |
| XX | | | | |
| PR | 06-JUL-1999; 98US-00110938. | | | |
| PR | 13-JUL-1998; 98US-00114666. | | | |
| PR | 13-JUL-1998; 98US-009389P. | | | |
| PR | 12-AUG-1998; 98US-00132968. | | | |
| PR | 18-AUG-1998; 98US-00136514. | | | |
| PR | 11-SEP-1998; 98US-0093999P. | | | |
| XX | | | | |
| PA | (SCHERING CORP. | | | |
| XX | | | | |
| PI | Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, German DM; | | | |
| PI | Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA; | | | |
| PI | Bazan JF, Mahony D, Lee EM; | | | |
| XX | | | | |
| DR | WPI; 2000-171015/15. | | | |
| XX | | | | |
| PT | New isolated mammalian genes, used to develop products for treating e.g. immune, inflammatory or allergic abnormalities, cancers or degenerative conditions. | | | |
| XX | | | | |
| PS | Disclosure; Page 208-209; 218pp; English. | | | |
| XX | | | | |
| CC | The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGm); the TNF (tumour necrosis factor receptor family)-related proteins HsTnfr84, HsTnfr37R and RANKL; human CC chemokine HCCs; human deubiquitinating proteins Dub1 and Dub12; human MD-1 and human murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin Cc2; cDNAs encoding these proteins, and antibodies against these proteins The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or substrates cellular interactions (e.g., induce or prevent trafficking, proliferation, or | | | |
| CC | | | | |

CC differentiant in various cellular processes such as the deubiquitination of
 CC proteins or cell cycle regulation. The products can be used for treating
 CC medical conditions such as immune, inflammatory or allergic disorders, or
 CC abnormal cellular proliferation, for example, cancers or degenerative
 CC conditions. They can be used to modulate immune responses in disease
 CC states e.g., autoimmune disorders, including rheumatoid arthritis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role.
 Sequences AA^Y77463-Y⁷⁷⁴⁶⁴, AAY⁷⁷⁴⁷⁴-Y⁷⁷⁴⁷⁵ and AAY⁷⁷⁴⁸⁴ represent primate
 CC proteins of undefined function. AA^Y77462 and AA^Y77481 are rodent proteins
 CC of undefined function, and AA^Y77482 is an avian protein of undefined
 CC function. These sequences are given in the sequence listing but are not
 CC referred to in the remainder of the specification.

SQ Sequence 162 AA;

Query Match 71.1%; Score 613; DB 3; Length 162;
 Best Local Similarity 66.7%; Pred. No. 8.5e-63; Gaps 0;
 Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

| | | |
|----|----------------------------------------------------------------|-----|
| QY | 1 MKGFTATLFWLTLIFPSCSGGGKAWTHVVSQSDGLEVLQYSCQDLODFGSFVKECSK | 60 |
| Db | 1 MKGFTATLFWLTLIFPSCSGGGKAWTHVVSQSDGLEVLQYSCQDLODFGSFVKECSK | 60 |
| QY | 61 QIKSNNINRGPILREDIKEFLFDALMSQGSVNLNSYPCIAALPKFSFCGRKKEQI | 120 |
| Db | 61 QIKSNNINRGPILRDIDTIRKFLFDITIMAKGSSILNTSYPLCEDQPKESFCGRKKEQI | 120 |
| QY | 121 YYAGVNNNPETIGGEYQNLSEYTERSTVCAANATMCS | 162 |
| Db | 121 YYAGVNNNPGLDVPOGEYQLLLELYNNENRATVACANATVSS | 162 |

RESULT 9

| | | |
|----|-------------------------------------------------------------------------|----------------------------|
| ID | ABU61846 | standard; protein; 162 AA. |
| XX | ABU61846; | |
| AC | ABU61846; | |
| XX | | |
| DT | 15-AUG-2003 | (first entry) |
| XX | | |
| DE | Mouse MD1. | |
| XX | | |
| KW | Mouse; MD1; cell development; tissue culture development. | |
| XX | | |
| OS | Mus sp. | |
| XX | | |
| PN | US2003028005-A1. | |
| XX | | |
| PD | 06-FEB-2003. | |
| XX | | |
| PR | 11-AUG-1999; | 99US-00372348. |
| XX | | |
| PR | 12-AUG-1998; | 98US-0096328P. |
| XX | | |
| PA | (BAZA/) | BAZAN J F. |
| XX | | |
| PI | Bazan J F; | |
| XX | | |
| DR | WPI; | 2003-466159/44. |
| XX | | |
| PT | New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or | |
| PT | rodent MD2 polypeptide, useful for modulating physiology or development | |
| PT | of a cell or tissue culture cells. | |
| XX | | |
| PS | Disclosure; Page 18; 77pp; English. | |
| XX | | |
| CC | The invention relates to a novel chemokine, de-ubiquitination or cell | |
| CC | surface protein. The composition is useful for modulating physiology or | |
| CC | development of a cell or tissue culture cells. The present sequence | |
| CC | represents the amino acid sequence of mouse MD1. | |

PS Disclosure; Page 210-211; 218PP; English.
 XX
 CC The invention relates to a number of primate and/or rodent proteins, and
 CC the genes which encode them. The invention encompasses human dendritic
 CC cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor)
 CC receptor family-related proteins HDEA84, HSLWD3TR and RANL; human CC
 CC chemokine HCC5; human deubiquitinating proteins Dub1 and Dub 12; human
 CC MD-1 and human and murine MD-2 proteins, which exhibit the properties of
 CC ligands for proteins comprising a leucine-rich motif (LRR); human cyclin
 CC B2; cDNAs encoding these proteins; and antibodies against these proteins.
 CC The proteins can be used for modulating the physiology or development of
 CC a cell. They can be used to mediate uptake of substrates (e.g.,
 CC prostaglandin-like molecules) to modulate cellular
 CC interactions (e.g., induce or prevent trafficking, proliferation, or
 CC differentiation of cells); or are intracellular proteins which are
 CC important in various cellular processes such as the deubiquitination of
 CC proteins or cell cycle regulation. The products can be used for treating
 CC medical conditions such as immune, inflammatory or allergic disorders, or
 CC abnormal cellular proliferation, for example, cancers or degenerative
 CC conditions. They can be used to modulate immune response in disease
 states e.g., autoimmune disorders, including rheumatoid arthritis, as well
 CC as systemic lupus erythematosus. Hashimoto's autoimmune thyroiditis, as well
 CC as acute and chronic inflammatory responses in which T cell activation,
 CC expansion, and/or immunological T cell memory play an important role.
 CC Sequences AAY77463-Y77464, AAY77474-Y77475 and AAY77481 are rodent proteins
 CC proteins of undefined function. AAY77462 and AAY77482 are avian protein
 CC of undefined function, and AAY77482 is an avian protein of undefined
 CC function. These sequences are given in the sequence listing but are not
 XX referred to in the remainder of the specification.

XX Sequence 160 AA;

Query Match 39.0%; Score 336; DB 3; Length 160;
 Best Local Similarity 44.4%; Pred. No. 1 4e-30;
 Matches 59; Conservative 26; Mismatches 48; Indels 0; Gaps 0;

QY 27 WPTHWVSDSGLEVLKQSCDPFDGFSVEKSKQLKSNNIRFGILREDKELFLDLA 86
 Db ||||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 22 WPTHTVKKEENLEIYVYKSCDPDQDFAFASIDRSDVTHTFDRAWYLRQSKEYAKVD 81
 QY 87 LMSQGSSVUNPSPYPICEALPKPSFCGRKGQIYVAGPVNNEFTIPOGSYQVLLY 146
 Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 82 LINGKTVISYSETLCPGLSKLIFCGKKGHLVYEGPITGKIEIPORDYTITARLN 141
 QY 147 EKRSTVACANATI 159
 Db |||:|||:|||:|||:|||:|||:
 82 LINGKTVISYSETLCPGLSKLIFCGKKGHLVYEGPITGKIEIPORDYTITARLN 141
 QY 147 EKRSTVACANATI 159
 Db |||:|||:|||:|||:
 142 EDRATVACADFTV 154

RESULT 13

AAY13929
 ID AAY13929 standard; protein; 160 AA.
 AC AAY13929;

XX DT 14-JUL-1999 (first entry)
 XX DE Mouse OMP106 protein.

XX OMP106: bacterial; viral; infection; cytokine activity; tissue formation;
 KW cell differentiation; immunostimulation; therapy;
 KW immunosuppression; haematopoiesis control; tissue repair.
 KW Mus musculus.
 OS XX
 PN WO9918205-A1.
 XX PD 15-APR-1999.
 XX PP 06-OCT-1998; 98MO-JP004515.
 XX PR 07-OCT-1997; 97JP-00274673.
 XX PA (ONO) ONO PHARM CO LTD.
 XX PI Honjo T, Kato K, Tada H;
 XX DR WPI: 1999-271269/23.
 DR N-PSDB; AIX36687, AIX36688.
 XX PT New polypeptides useful in the treatment of various diseases including
 PT bacterial and viral infections with cytokine activity.
 XX PS Claim 1; Page 36-37; 57pp; Japanese.

XX CC This sequence represents a OMP106 protein of the invention. The
 PA polyptides and their antibodies are applicable in drug compositions.
 XX CC

PI Bazan JF;
 XX DR WPI; 2003-466159/44.
 DR N-PSDB; ACAB2465.
 DR PT New composition comprising HCC5, Dub1, Dub12, Primate MD1 or MD2 or
 PT rodent MD2 polypeptide, useful for modulating physiology or development
 PT of a cell or tissue culture cells.
 XX PS Disclosure; Page 18; 77PP; English.
 XX CC The invention relates to a novel chemokine, de-ubiquitination or cell
 CC surface protein. The composition is useful for modulating physiology or
 CC development of a cell or tissue culture cells. The present sequence
 CC represents the amino acid sequence of chicken MD1
 XX SQ Sequence 160 AA;
 Query Match 39.0%; Score 336; DB 6; Length 160;
 Best Local Similarity 44.4%; Pred. No. 1 4e-30;
 Matches 59; Conservative 26; Mismatches 48; Indels 0; Gaps 0;
 QY 27 WPTHWVSDSGLEVLKQSCDPFDGFSVEKSKQLKSNNIRFGILREDKELFLDLA 86
 Db |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 22 WPTHTVKKEENLEIYVYKSCDPDQDFAFASIDRSDVTHTFDRAWYLRQSKEYAKVD 81
 QY 87 LMSQGSSVUNPSPYPICEALPKPSFCGRKGQIYVAGPVNNEFTIPOGSYQVLLY 146
 Db |||:|||:|||:|||:|||:|||:
 82 LINGKTVISYSETLCPGLSKLIFCGKKGHLVYEGPITGKIEIPORDYTITARLN 141
 QY 147 EKRSTVACANATI 159
 Db |||:|||:|||:
 142 EDRATVACADFTV 154

CC useful for treatment of various diseases including bacterial and viral
 CC infections with cytokine activity, and activities e.g. on cell
 CC proliferation/differentiation, immunostimulation/suppression, control of
 CC haemopoiesis, and tissue formation and repair. The proteins and
 CC antibodies have a wide spectrum of activities
 XX sequence 160 AA;

Query Match 12.3%; Score 106; DB 2; Length 160;
 Best Local Similarity 26.3%; Pred. No. 0.00084; Mismatches 61; Indels 16; Gaps 5;
 Matches 36; Conservative 24; MisMatches 61; Indels 16; Caps 5;

Qy 33 CSDSGLEVLYQSCDPLQ-DFGFSVEKCSQLKSNINIRPGILIREDIKEFLDIALMSQ 91
 Db 25 CNSSDAILISYSYCDHLKRPPISSCPCIRLGRGPFVHEFTPRGNKLYVNLFI--- 80
 Qy 92 SSVINFSYI---ICEALPKTSFCGRRKGQIYAGPVNNPEFTIPQGEVQVILE- 145
 Db 81 -SVNSIELPDKRKEVILCHGHDYDFCRALKGETNTSIPFSRGLIPFKGHRCVAIA 139

Qy 146 --TEKRSTACANATIM 160
 Db 140 GDTBEK--LFCLNFTII 154

RESULT 14
 ID AAB35928 standard; protein; 160 AA.
 AC AAB35928;
 XX DT 26-FEB-2001 (first entry)
 XX DE Murine MD-2 amino acid sequence.
 XX KW MD-2; immunosuppressant; allergy; asthma; atopic dermatitis; mouse;
 KW infection; prevention.
 OS XX Mus musculus.
 XX PR JP2000262290-A.
 XX PN XX 26-SEP-2000.
 XX PR 18-MAR-1999; 99JP-00073815.
 XX PR 16-MAR-1999; 99JP-00073815.
 XX PA (MITU) MITSUBISHI CHEM CORP.
 XX DR NPF; 2000-682118/67.
 XX DR N-PSDB; AAC63388.
 XX PT A new protein controlling the infection-preventing reaction against a
 PT microbe.
 XX PS Claim 2; Page 11-13; 14PP; Japanese.
 XX SQ This invention relates to a protein, MD-2, which controls an infection
 CC prevention reaction against a microbe. Protein and cDNA sequences
 CC AAC66387 - AAC66388 and AAB35927 - AAB35928 represent human and mouse MD-
 CC 2. MD-2 increases NFκB activation through TLR4 molecules. The protein
 CC has immunosuppressant, anti-allergy; antiarrhythmic and dermatological
 CC activity. The protein and the DNA can be used as a treating agent and a
 CC diagnostic agent for diseases such as autoimmune diseases, allergic
 CC diseases, asthma and atopic dermatitis
 XX Sequence 160 AA;

Query Match 12.3%; Score 106; DB 3; Length 160;
 Best Local Similarity 26.3%; Pred. No. 0.00084; Mismatches 61; Indels 16; Gaps 5;
 Matches 36; Conservative 24; MisMatches 61; Indels 16; Caps 5;

Qy 33 CSDSGLEVLYQSCDPLQ-DFGFSVEKCSQLKSNINIRPGILIREDIKEFLDIALMSQ 91
 Db 25 CNSSDAILISYSYCDHLKRPPISSCPCIRLGRGPFVHEFTPRGNKLYVNLFI--- 80
 Qy 92 SSVINFSYI---ICEALPKTSFCGRRKGQIYAGPVNNPEFTIPQGEVQVILE- 145
 Db 81 -SVNSIELPDKRKEVILCHGHDYDFCRALKGETNTSIPFSRGLIPFKGHRCVAIA 139

Qy 146 --TEKRSTACANATIM 160
 Db 140 GDTBEK--LFCLNFTII 154

RESULT 15
 ID AAY13931 standard; protein; 160 AA.
 XX AC AAY13931;
 XX DT 14-JUL-1999 (first entry)
 XX DB Human OMP106 protein.
 XX KW OMP106; bacterial; viral; infection; cytokine activity; tissue formation;
 KW cell proliferation; cell differentiation; immunostimulation; therapy;
 KW immunosuppression; haemopoiesis control; tissue repair.
 XX OS Homo sapiens.
 XX PN WO9918205-A1.
 XX PA (ONO) ONO PHARM CO LTD.
 XX PI Honjo T, Kato X, Tada H;
 XX DR WPI; 1999-277269/23.
 XX DR N-PSDB; AAX36691, AAX36692.
 XX PT New polypeptides useful in the treatment of various diseases including
 PT bacterial and viral infections with cytokine activity.
 XX PR 06-OCT-1998; 98WO-JP004515.
 XX PR 07-OCT-1997; 97JP-00274673.
 XX PA (ONO) ONO PHARM CO LTD.
 XX PI Honjo T, Kato X, Tada H;
 XX DR WPI; 1999-277269/23.
 XX DR N-PSDB; AAX36691, AAX36692.
 XX PT This sequence represents a OMP106 protein of the invention. The
 CC polypeptides and their antibodies are applicable in drug compositions,
 CC useful for treatment of various diseases including bacterial and viral
 CC infections with cytokine activity, and activities e.g. on cell
 CC proliferation/differentiation, immunostimulation/suppression, control of
 CC haemopoiesis, and tissue formation and repair. The proteins and
 CC antibodies have a wide spectrum of activities
 XX Sequence 160 AA;

Query Match 11.8%; Score 101.5; DB 2; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0028; Mismatches 70; Indels 11; Gaps 3;
 Matches 34; Conservative 26; MisMatches 70; Indels 11; Gaps 3;

Qy 4 FTATPLWTFIFPCSGGGKAMPTHVCSDSLEVLVQSCDPLQ-DFGFSVEKCSQL 62
 Db 6 FPFSTLP--SSIFT-----EAKQYWVNSDASITYCDNQYPISSINVPCEIK 55

Qy 63 KSNINIRPGILIREDIKEFLDIALMSQSSVNLFSVPCALPKTSFCGRRKGQIY 122
 Db 56 GSKGLIHPFIPPRDKQYVNLITVNTMLPKRKEVICRGSDDYDFCRALKGETNT 115

Qy 123 AGPVNNPEFTIPQGYVQIE 143

Thu Apr 29 15:51:26 2004

ub-09-899-917-2.rag

Page 9

Db 116 TISFSFKGKIKFSGKGKYKVVE 136

Search completed: April 29, 2004, 15:22:20
Job time : 60 secs

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OM protein - protein search, using sw model

Run on: April 29, 2004, 15:21:06 ; Search time 23 Seconds
 (without alignments)

363.626 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862

Sequence: I MKGFTATPIWTLIFPSSG.....ELYTERKSTVACANATIMCS 162

Scoring table: BLOSUM62 , Gapop 10.0 , Gapext 0.5

Searched: Gapext 0.5

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AK:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB_Pep: *

2: /cgn2_6/ptodata/2/iaa/6A_COMB_Pep: *

3: /cgn2_6/ptodata/2/iaa/6B_COMB_Pep: *

4: /cgn2_6/ptodata/2/iaa/PCTM_Comb_Pep: *

5: /cgn2_6/ptodata/2/iaa/backles1.Pep: *

6: /cgn2_6/ptodata/2/iaa/backles1.Pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | % | Match Length | DB ID | Description |
|------------|-------|-------|------|-----------------|----------------------|---------------------|
| 1 | 862 | 100.0 | 162 | 3 | US-08-994-962-2 | Sequence 2, Appli |
| 2 | 344 | 39.9 | 133 | 3 | US-08-994-962-3 | Sequence 3, Appli |
| 3 | 94 | 10.9 | 60 | 3 | US-08-994-962-17 | Sequence 17, Appli |
| 4 | 73.5 | 8.5 | 264 | 3 | US-08-968-644-16 | Sequence 16, Appli |
| 5 | 73.5 | 8.5 | 264 | 3 | US-08-441-189-16 | Sequence 16, Appli |
| 6 | 73.5 | 8.5 | 264 | 3 | US-08-463-54-16 | Sequence 16, Appli |
| 7 | 73.5 | 8.5 | 442 | 1 | US-08-20-151-22 | Sequence 22, Appli |
| 8 | 73.5 | 8.5 | 442 | 1 | US-08-410-118-22 | Sequence 22, Appli |
| 9 | 73.5 | 8.5 | 442 | 3 | US-08-471-446-22 | Sequence 22, Appli |
| 10 | 73.5 | 8.5 | 442 | 6 | 5470718-3 | Patent No. 5470718 |
| 11 | 73 | 8.5 | 787 | 4 | US-07-252-991A-26468 | Sequence 26468, A |
| 12 | 71.5 | 8.3 | 442 | 6 | 5470718-2 | Patent No. 5470718 |
| 13 | 71 | 8.2 | 668 | 1 | US-08-530-950-13 | Sequence 13, Appli |
| 14 | 71 | 8.2 | 668 | 3 | US-09-19-879-13 | Sequence 13, Appli |
| 15 | 71 | 8.2 | 668 | 4 | US-09-057-009-13 | Sequence 13, Appli |
| 16 | 69.5 | 8.1 | 184 | 4 | US-09-384-162-12 | Sequence 12, Appli |
| 17 | 69 | 8.0 | 1012 | 4 | US-09-285-385C-4 | Sequence 4, Appli |
| 18 | 68 | 7.9 | 294 | 4 | US-08-252-991A-27242 | Sequence 27242, A |
| 19 | 68 | 7.9 | 459 | 1 | US-08-336-618-12 | Sequence 12, Appli |
| 20 | 68 | 7.9 | 459 | 1 | US-08-336-618-26 | Sequence 26, Appli |
| 21 | 68 | 7.9 | 857 | 1 | US-07-17-331F-2 | Sequence 331, Appli |
| 22 | 67.5 | 7.8 | 204 | 4 | US-08-134-001C-3617 | Sequence 4, Appli |
| 23 | 67.5 | 7.8 | 458 | 1 | US-08-336-618-24 | Sequence 227, Appli |
| 24 | 67.5 | 7.8 | 844 | 4 | US-08-561-805-227 | Sequence 8, Appli |
| 25 | 66.5 | 7.7 | 372 | 1 | US-08-597-236-8 | Sequence 8, Appli |
| 26 | 66.5 | 7.7 | 1 | US-08-468-558-5 | Sequence 5, Appli | |
| 27 | 66.5 | 7.7 | 793 | 2 | US-08-468-558-5 | Sequence 2, Appli |

ALIGNMENTS

Printed by Dr. Steffie Eric K.

RESULT 1
 US-09-994-962-2
 ; Sequence 2, Application US/08994962
 Patent No. 6284466

GENERAL INFORMATION:
 APPLICANT: Olsen, Henrik S.
 TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stern, Kessler Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Ave., NW, Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/994,962
 FILING DATE: Herewith
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,869

FILING DATE: 20-DEC-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/037,388

FILING DATE: 07-FEB-1997

CLASSIFICATION: 202-371-2540

ATTORNEY/AGENT INFORMATION:
 NAME: Steffie, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0440002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 162 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-994-962-2

Query Match 100.0%; Score 862; DB 3; Length 162;
 Best Local Similarity 100.0%; Pred. No. 8e-100;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKFTATLFLWMTLIFPSCSGGGKAWPHTWCSSGLEVIYQSCDPLQDFGSVEKSK 60
Db 1 MGKFTATLFLWMTLIFPSCSGGGKAWPHTWCSSGLEVIYQSCDPLQDFGSVEKSK 60

QY 61 QKSNINIRFGILREDIKEIYLFLDAMSQSISVLSYPICEAALPKFSFCGRKGEOI 120
Db 61 QKSNINIRFGILREDIKEIYLFLDAMSQSISVLSYPICEAALPKFSFCGRKGEOI 120

RESULT 2
US-08-994-962-3

Sequence 3, Application US/08994962

Patent No. 628486

GENERAL INFORMATION:

APPLICANT: Olsen, Henrik S.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/994,962

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/033, 869

FILING DATE: 20-DEC-1996

CLASSIFICATION:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/037, 388

FILING DATE: 07-FEB-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488-0440002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

FAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 60 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-994-962-3

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

Query Match 39.9%; Score 344; DB 3; Length 60;
Best Local Similarity 33.3%; Pred. No. 0.00027; Mismatches 43; Conservative 3; Indels 70; Gaps 11; Matches 43; Conservative 3; Mismatches 13; Indels 70; Gaps 11;

QY 27 WPTHRVCSSGGLLEVLYQSCDPLQDFGSVEKSKQKLSNINIRFGILREDIKEIYLFLDAMSQSISVLSYPICEAALPKFSFCGRKGEOIYAGPVNPETIPOGEYQVLELYT 146
Db 1 WPTHRVCSSGGLLEVLYQSCDPLQDFGSVEKSKQKLSNINIRFGILREDIKEIYLFLDAMSQSISVLSYPICEAALPKFSFCGRKGEOIYAGPVNPETIPOGEYQVLELYT 146

QY 1 WPTHTVCKEERVYKSCDQQPAPAFSIDSVDTHFDIRAMVLRQSIRELYAKD 60
Db 30 -----GVLSCLEFG--KGE--YYGP-----IPQG-----YL 52

QY 147 EKRSTVACA 155
Db 53 ER--TVACA 59

87 LMSQGSSVLNSYPICEAALPKFSFCGRKGEOIYAGPVNPETIPOGEYQVLELYT 146

RESULT 4
US-08-969-644-16
Sequence 16, Application US/08969644
; Patent No. 6096519
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; APPLICANT: Tecce, Mario F.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,644
; FILING DATE: 13-Nov-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,152
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-969-644-16
Query Match 8.5%; Score 73.5; DB 3; Length 264;
Best Local Similarity 27.6%; Pred. No. 0.83;
Matches 35; Conservative 13; Mismatches 50; Indels 29; Gaps 5;
Qy 10 LWTLLPPSCSGGGGGKAWMPTHVVCSDS--GLEVLYQSCDPHQDFGSVEKCSQQLKSN 66
Db 1 LHTLVPCSKKGIGKTTLSLNGNLQAQPLGKKVLADDP-----QSNL 45
Qy 67 NIRFGTILRDIKEFLDLMMSQGSSVNVSPYICEAA---LPKTSFCGRKGQEYI 121
Db 46 SSGLGASVRSQKGLH-DIVVTSNDLSI---ICETKDSVNLIPASFSQFRELDI 99
Qy 122 YAGPYNN 128
Db 100 HRGPSNN 106

RESULT 5
US-08-444-189-16
Sequence 16, Application US/08444189
; Sequence 16, Application US/08444189
; Patent No. 6110705
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,189
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,528
; FILING DATE:
; APPLICATION NUMBER: US/07/991,512
; FILING DATE:
; APPLICATION NUMBER: US/07/661,820
; FILING DATE:
; APPLICATION NUMBER: IT MI 91A000314
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELEPHONE: 703-241-1300
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-189-16
Query Match 8.5%; Score 73.5; DB 3; Length 264;
Best Local Similarity 27.6%; Pred. No. 0.83;
Matches 35; Conservative 13; Mismatches 50; Indels 29; Gaps 5;
Qy 10 LWTLLPPSCSGGGGGKAWMPTHVVCSDS--GLEVLYQSCDPHQDFGSVEKCSQQLKSN 66
Db 1 LHTLVPCSKKGIGKTTLSLNGNLQAQPLGKKVLADDP-----QSNL 45
Qy 67 NIRFGTILRDIKEFLDLMMSQGSSVNVSPYICEAA---LPKTSFCGRKGQEYI 121
Db 46 SSGLGASVRSQKGLH-DIVVTSNDLSI---ICETKDSVNLIPASFSQFRELDI 99
Qy 122 YAGPYNN 128
Db 100 HRGPSNN 106

RESULT 6
US-08-468-544-16
Sequence 16, Application US/08468544

PATENT NO. 6348563
 GENERAL INFORMATION:
 APPLICANT: Ratti, Giulio
 APPLICANT: Comanducci, Maurizio
 APPLICANT: Tecce, Mario F.
 APPLICANT: Giuliani, Marzia M.
 TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
 TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
 TITLE OF INVENTION: THEM: RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
 TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
 STREET: 301 N. Washington Street
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22046-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/468,544
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/661,820
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: ITMI 91A00031-4
 FILING DATE: 07-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svensson, Leonard R.
 REGISTRATION NUMBER: 30,330
 REFERENCE DOCKET NUMBER: 1267-202P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-241-1300
 TELEFAX: 703-241-2848
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 264 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-468-544-16
 Query Match 8.5%; Score 73.5; DB 1; Length 442;
 Best Local Similarity 27.6%; Pred. No. 0.83; DB 3; Length 264;
 Matches 35; Conservative 13; Mismatches 50; Indels 29; Gaps 5;
 QY 10 LWTIIPSCGGGGKAWPAUTHVCCSDS--GLEVLYQSCDPQLQDFGSVEKCSQKLN 66
 Db 1 LHTLIVFCERKGKGKTTTSLANGVNLQFLGKRYLADLP-----QSNT 45
 QY 2 KGFTMILFLMLLIFPSCGGGGKAWPAUTHVCCSDSGLGEVLYQSCDPQLQDFGSVEKCSQK 61
 Db 161 KTYSSRL-TWPKIMTC-----ATPH-----DYSYMKCNPKUSFAMDE---- 199
 QY 62 LKSNINTRFGITI--LREDIKEFLFDALMSQGSVLT-----NFSYPICEAA 105
 Db 200 -RSDILWQASLITMAETDDELGLVLAAPAHSAQGLYRVIEEDGRRIYDFSTVPSR 258
 QY 106 LP-----KFPFCGRKRGQIYVAGVNN---PPTIPOGEGYVQILEY 145
 Db 259 CFPIAFFLNFGNPDRCKTPEQYSRGEVFTTRFLGEFPNPFOGBMWIVWKFW 307
 RESULT 7
 Sequence 22, Application US/08220151
 GENERAL INFORMATION:
 APPLICANT: Paoletti, Enzo
 APPLICANT: Limbach, Keith J.
 TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
 NUMBER OF SEQUENCES: 128
 CORRESPONDENCE ADDRESS:
 ADDRESSE: CURTIS, MORRIS & SAFORD, P.C.
 STREET: 530 FIFTH AVENUE, 25TH FLOOR
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
 NUMBER OF SEQUENCES: 91
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Curtiss, Morris & Safford
 STREET: 550 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/220/151
 FILING DATE: 30-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Frimer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2540
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
 FRAGMENT TYPE: N-terminal
 US-08-220-151-22
 Query Match 8.5%; Score 73.5; DB 1; Length 442;
 Best Local Similarity 25.4%; Pred. No. 1.7; DB 3; Length 442;
 Matches 43; Conservative 17; Mismatches 62; Indels 47; Gaps 8;
 QY 2 KGFTMILFLMLLIFPSCGGGGKAWPAUTHVCCSDSGLGEVLYQSCDPQLQDFGSVEKCSQK 61
 Db 161 KTYSSRL-TWPKIMTC-----ATPH-----DYSYMKCNPKUSFAMDE---- 199
 QY 62 LKSNINTRFGITI--LREDIKEFLFDALMSQGSVLT-----NFSYPICEAA 105
 Db 200 -RSDILWQASLITMAETDDELGLVLAAPAHSAQGLYRVIEEDGRRIYDFSTVPSR 258
 QY 106 LP-----KFPFCGRKRGQIYVAGVNN---PPTIPOGEGYVQILEY 145
 Db 259 CFPIAFFLNFGNPDRCKTPEQYSRGEVFTTRFLGEFPNPFOGBMWIVWKFW 307
 RESULT 8
 Sequence 22, Application US/08413118
 GENERAL INFORMATION:
 APPLICANT: PAOLETTI, ENZO
 APPLICANT: LIMBACH, KEITH J.
 TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
 NUMBER OF SEQUENCES: 128
 CORRESPONDENCE ADDRESS:
 ADDRESSE: CURTIS, MORRIS & SAFORD, P.C.
 STREET: 530 FIFTH AVENUE, 25TH FLOOR
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/413,118
 FILING DATE: 29-MAR-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/220,151
 FILING DATE: 30-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: FROMMER, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45310-2670
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-0712
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: N-terminal
 US-08-413-118-22

Query Match 8.5%; Score 73.5; DB 1; Length 442;
 Best Local Similarity 25.4%; Pred. No. 1,7; Mismatches 62; Indels 47; Gaps 8;
 Matches 43; Conservative 17; Length 442;

Qy 2 KGFTATLFWTLTPSCGGGCGKAWPTWVCSDCDPLQDFGSVERKCSKQ 61
 Db 161 KTVSRL-TWFKIMPTC---ATPIH-----DVSYMKNPKLSFAMCDE---- 199

Qy 62 LKSNINIRGGI-LREDIKEFLDLAAMSQSSVL-----NFSYPICEAA 105
 Db 200 -RSDLIWQSLITMAETDELGLVLAAPAHSGLYRRVIEIDGRRIYTDFSVTIPSER 258

Qy 106 LP----KPSFCGRRKGQQIYAGPVNN---PEFTIPOGEYQVILEY 145
 Db 259 CPIAFLENFGNPDRCRKTPBQYSRGEVTRRFLGEFNFFQGEHMWTWKF 307

RESULT 9
 US-08-473-446-22
 Sequence 22, Application US/08473446
 PRIORITY NUMBER: 6011542
 GENERAL INFORMATION:
 APPLICANT: PAOLETTI, ENZO
 APPLICANT: LIMBACH, KEITH J.
 TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
 NUMBER OF SEQUENCES: 128
 CORRESPONDENCE ADDRESS:
 ADDRESS: CUTTER, MORRIS & SAFFORD, P.C.
 STREET: 530 FIFTH AVENUE, 25TH FLOOR
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,446
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/413,118
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: FROMMER, WILLIAM S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 45310-2670
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-0712
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 442 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: N-terminal
 US-08-473-446-22

Query Match 8.5%; Score 73.5; DB 3; Length 442;
 Best Local Similarity 25.4%; Pred. No. 1,7; Mismatches 62; Indels 47; Gaps 8;
 Matches 43; Conservative 17; Length 442;

Qy 2 KGFTATLFWTLTPSCGGGCGKAWPTWVCSDCDPLQDFGSVERKCSKQ 61
 Db 161 KTVSRL-TWFKIMPTC---ATPIH-----DVSYMKNPKLSFAMCDE---- 199

Qy 62 LKSNINIRGGI-LREDIKEFLDLAAMSQSSVL-----NFSYPICEAA 105
 Db 200 -RSDLIWQSLITMAETDELGLVLAAPAHSGLYRRVIEIDGRRIYTDFSVTIPSER 258

Qy 106 LP----KPSFCGRRKGQQIYAGPVNN---PEFTIPOGEYQVILEY 145
 Db 259 CPIAFLENFGNPDRCRKTPBQYSRGEVTRRFLGEFNFFQGEHMWTWKF 307

RESULT 10
 US-08-473-446-22
 Sequence 22, Application US/08473446
 PRIORITY NUMBER: 6011542
 GENERAL INFORMATION:
 APPLICANT: O'CALLAGHAN, DENNIS J.
 TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
 NUMBER OF SEQUENCES: 8
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/954,417
 FILING DATE: 30-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 561,553
 FILING DATE: 01-AUG-1990
 SEQ ID NO:3:
 LENGTH: 442
 5470718-3

Query Match 8.5%; Score 73.5; DB 6; Length 442;
 Best Local Similarity 25.4%; Pred. No. 1,7; Mismatches 62; Indels 47; Gaps 8;
 Matches 43; Conservative 17; Length 442;

Qy 2 KGFTATLFWTLTPSCGGGCGKAWPTWVCSDCDPLQDFGSVERKCSKQ 61
 Db 161 KTVSRL-TWFKIMPTC---ATPIH-----DVSYMKNPKLSFAMCDE---- 199

Qy 62 LKSNINIRGGI-LREDIKEFLDLAAMSQSSVL-----NFSYPICEAA 105
 Db 200 -RSDLIWQSLITMAETDELGLVLAAPAHSGLYRRVIEIDGRRIYTDFSVTIPSER 258

Qy 106 LP----KPSFCGRRKGQQIYAGPVNN---PEFTIPOGEYQVILEY 145
 Db 259 CPIAFLENFGNPDRCRKTPBQYSRGEVTRRFLGEFNFFQGEHMWTWKF 307

RESULT 11
 US-08-252-991A-26468
 Sequence 26459, Application US/08252991A
 PARENT NO. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.

STATE: MA
COUNTRY: USA
ZIP: 01110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #11.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-13

Query Match Score 71; DB 3; Length 668;
Best Local Similarity 24.3%; Pred. No. 64; Mismatches 61; Indels 18; Gaps 5;
Matches 33; Conservative 24; Mismatches 61; Indels 18; Gaps 5;

QY 28 PTHWVCCDSGLEVLVYQSCDPIQDFGFSVEKCKSKLNSNTRFGILREDIKEFLIDAL 87
Db 48B PTNLCSAN-----QGTVKLCDPGVSGNLVSLAKTNIGCQ-SMAPERIKSINPDRAT 540

QY 88 MSQSSVNLNPSPYCEAALPKPSFCGRKRGEOQY--YAGPVNNEFTIPQGY----- 138
Db 541 YTVQSDIWSLGLSIGLLEMALGRPY-PPTEDYDNIFSQLISAVUDGPPRPLPSDKFSSDAQDF 599

QY 139 -QVILELYERKSTVA 153
Db 600 VSLCLQKIPERRPRYIA 615

Search completed: April 29, 2004, 15:23:47
Job time : 23 secs

RESULT 15
US-09-057-009-13
Sequence 13; Application US/09057009
; Sequence 13; Application US/09057009
; Patent No. 6541605
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raineaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE- 'STRESS-' AND
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #11.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,009
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6541605 Relevant
TOPOLOGY: linear
US-09-057-009-13

Query Match Score 71; DB 4; Length 668;
Best Local Similarity 24.3%; Pred. No. 64; Mismatches 61; Indels 18; Gaps 5;
Matches 33; Conservative 24; Mismatches 61; Indels 18; Gaps 5;

QY 28 PTHWVCCDSGLEVLVYQSCDPIQDFGFSVEKCKSKLNSNTRFGILREDIKEFLIDAL 87
Db 48B PTNLCSAN-----QGTVKLCDPGVSGNLVSLAKTNIGCQ-SMAPERIKSINPDRAT 540

QY 88 MSQSSVNLNPSPYCEAALPKPSFCGRKRGEOQY--YAGPVNNEFTIPQGY----- 138
Db 541 YTVQSDIWSLGLSIGLLEMALGRPY-PPTEDYDNIFSQLISAVUDGPPRPLPSDKFSSDAQDF 599

QY 139 -QVILELYERKSTVA 153
Db 600 VSLCLQKIPERRPRYIA 615

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 29, 2004, 15:23:51 ; Search time 42 Seconds (without alignments)
1069.160 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862

Sequence: 1 MKGFTATLFLNWLIPFSSCG..... ELYTEKRSTVACANATIMCS 162

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of bits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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11: /cgn2_6/prodata/2/pupaa/US09_PUBCOMB.pep: *
12: /cgn2_6/prodata/2/pupaa/US09_NEW_PUB.pep: *
13: /cgn2_6/prodata/2/pupaa/US09_PUBCOMB.pep: *
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17: /cgn2_6/prodata/2/pupaa/US60_NEW_PUB.pep: *
18: /cgn2_6/prodata/2/pupaa/US60_PUBCOMB.pep: *

'Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-09-899-917-2
; Sequence 2, Application US/09899917
; Patent No. US20020119552A1
; GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-899,917
FILING DATE: 09-JUL-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/994,962
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REFERENCE DOCKET NUMBER: 1488-0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-571-2600
TELEFAX: 202-571-2540
INFORMATION FOR SEQ ID NO: 2:

Sequence 29, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 19, Appli
Sequence 27, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 29, Appli
Sequence 1, Appli
Sequence 23, Appli
Sequence 7, Appli
Sequence 26, Appli
Sequence 17, Appli
Sequence 199134, Appli
Sequence 214931, Appli
Sequence 199134, Appli
Sequence 77325, A

SEQUENCE CHARACTERISTICS:
 LENGTH: 162 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2;
 US-09-899-917-2

Query Match 100.0%; Score 862; DB 9; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1. 8e-93; Mismatches 0; Indels 0; Gaps 0;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60
 Db 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60

Qy 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60
 Db 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60

Qy 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162
 Db 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162

RESULT 2
 Sequence 13, Application US/10000056
 Publication No. US20020086364A1
 GENERAL INFORMATION:

APPLICANT: HONJO, TASAKU
 APPLICANT: KATO, KEIZO
 APPLICANT: TADA, KEIZO

TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM

FILE REFERENCE: Q5871
 CURRENT APPLICATION NUMBER: US/10/000, 066

CURRENT FILING DATE: 2001-12-04
 PRIOR APPLICATION NUMBER: 09/529, 064

PRIOR FILING DATE: 2000-04-17
 PRIOR APPLICATION NUMBER: PCT/JP98/04515

PRIOR FILING DATE: 1998-10-05
 PRIOR APPLICATION NUMBER: HEI-9-274673

PRIOR FILING DATE: 1997-10-07
 NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13
 LENGTH: 162
 TYPE: PRT

ORGANISM: Homo sapiens
 US-10-000-056-13

Hand date

APPLICANT: Hedrick, Joseph A.
 APPLICANT: Wang, Luquan
 APPLICANT: Zlotnik, Albert
 APPLICANT: Murgolo, Nicholas J.
 APPLICANT: Greene, Jonathan R.
 APPLICANT: Johnston, James A.

FILE REFERENCE: DX084K(2d)
 CURRENT APPLICATION NUMBER: US/09/372, 348A
 CURRENT FILING DATE: 1999-08-11
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.0

SSO ID NO 19
 LENGTH: 162
 TYPE: PRT

ORGANISM: primate
 US-09-372-348-19

Query Match 98.6%; Score 850; DB 10; length 162;
 Best Local Similarity 98.8%; Pred. No. 4. 8e-92; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60
 Db 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60

Qy 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60
 Db 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60

Qy 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162
 Db 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162

RESULT 4
 Sequence 27, Application US/09/372348A
 Publication No. US20030028005A1
 GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.
 APPLICANT: Wang, Luquan
 APPLICANT: Zlotnik, Albert
 APPLICANT: Murgolo, Nicholas J.

APPLICANT: Greene, Jonathan R.
 APPLICANT: Johnston, James A.

FILE REFERENCE: DX084K(2d)

CURRENT APPLICATION NUMBER: US/09/372, 348A
 CURRENT FILING DATE: 1999-08-11

NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.0

TYPE: PRT

ORGANISM: rodent
 US-09-372-348-27

Query Match 71.1%; Score 613; DB 10; Length 162;
 Best Local Similarity 66.7%; Pred. No. 5e-64; Mismatches 32; Indels 0; Gaps 0;

Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60
 Db 1 MKGFTATLFLWTIIPPSCSGGGGKAWTHVWSDSGLEVLQSCDPLQDFGSVEKCSK 60

Qy 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60
 Db 61 QLKSNINIRFGILREDIKEFLDIALMSQSGLVYQSCDPLQDFGSVEKCSK 60

Qy 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162
 Db 121 YVAGPVNNPFTIPOGEYQVLLYTERSTVACANATMCS 162

RESULT 3
 Sequence 19, Application US/09/72348A
 Publication No. US20030028005A1
 GENERAL INFORMATION:

APPLICATION NUMBER: 08/994,962
 FILING DATE: <Unknown>
 PRIORITY NUMBER: US 60/037,388

RESULT 5
 US-10-000-066-10
 ; Sequence 10, Application US/10000066

GENERAL INFORMATION:

APPLICANT: HONJO, TSURUJ

APPLICANT: KATO, KEIZO

APPLICANT: TADA, HIDEAKI

TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM

FILE REFERENCE: Q58771
 CURRENT APPLICATION NUMBER: US/10/000,066

CURRENT FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: 09/529,064

PRIOR FILING DATE: 2000-04-17
 * PRIOR APPLICATION NUMBER: PCT/JP98/04515

PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: HEI-9-274673

PRIOR FILING DATE: 1997-10-07
 NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 10

LENGTH: 162

TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-000-066-10

Query Match 71.1%; Score 613; DB 12; Length 162;
 Best Local Similarity 65.7%; Pred. No. 5e-64; Mismatches 32; Indels 0; Gaps 0;
 Matches 108; Conservative 22; MisMatches 32; Length: 162

Qy 1 MKGFTATLFLWLTIPPCGGGKAKWPHVCSDSGLVLYQSCDPLQDFGSGVCKSK 60
 Db 1 MNGVARALLWLINSPPSSDHGSENGWPKHTACNSGGLGIVVQSCDPLODFGSIQCSK 60

Qy 61 QLSMINIRGILIREDIKLFIDALMQGSVINFSPICAAALPFSFCRRKRSQI 120
 Db 61 QIQSNLNRIGFILRQDIRKLDTIMAKGSINVSYPCLCEDQPKFSCRRKRSQI 120

Qy 121 YVAGPVNPETIPQGEIQVLLYTERKSTIVACANATMCS 162
 Db 121 YYAGPYVNPGLDVPQGEYQVLLENTRAVACANATVSS 162

RESULT 6
 US-9-899-917-3
 ; Sequence 3, Application US/09899917
 ; Patent No. US2002011952A1

GENERAL INFORMATION:

APPLICANT: Olsen, Henrik S.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Ave., NW, Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/899,917
 FILING DATE: 09-Jul-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 SEQ ID NO: 10

APPLICATION NUMBER: 08/994,962
 FILING DATE: <Unknown>
 PRIORITY NUMBER: US 60/037,388

RESULT 7
 US-09-372-348-29
 Sequence 29, Application US/09312348A
 Publication No. US20030028005A1

GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.

APPLICANT: Wang, Duquan

APPLICANT: Zlotnik, Albert

APPLICANT: Murgolo, Nicholas J.

APPLICANT: Greene, Jonathan R.

APPLICANT: Johnston, James A.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods

FILE REFERENCE: DX08842D

CURRENT APPLICATION NUMBER: US/09/372,348A

CURRENT FILING DATE: 1999-08-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 29

LENGTH: 160

TYPE: PRT
 ; ORGANISM: aves
 US-09-372-348-29

Query Match 39.0%; Score 336; DB 10; Length 160;
 Best Local Similarity 44.4%; Pred. No. 2.8e-31; Mismatches 48; Indels 0; Gaps 0;
 Matches 59; Conservative 26; MisMatches 48; Length: 160

Qy 27 WPRTHVCSDSGLVLYQSCDPLQDFGSGVCKSKQLKNINIRGIFTLREDITKELFLDA 86
 Db 22 WPRTVCKENLBIYKSCDPOODFAFSIDRCSDVTHTFDRAAMVLQSICKLYAKD 81

Qy 87 LMSQGSSVINFSYPICAAALPFSFCRRKAGQIYVAGPVNPETIPQGEQVLLY 146
 Db 82 LINGKTIVLVSYSITLCGPGLSLKIFCGKKGEHLYVEGPITLGIKEIPQDDYTARTLN 141

Query Match 11.8%; Score 101.5; DB 10; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0015; Indels 11; Gaps 3;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 147 ERSTVACANATI 159
 Db 142 EDRATVACADFTV 154

RESULT 8

US-10-000-066-1
 Sequence 1 Application US/10000066
 Publication No. US20020086364A1
 GENERAL INFORMATION:
 APPLICANT: HONJO, TASUKU
 APPLICANT: KATO, KEIZO
 APPLICANT: TADA, HIDENAKI
 TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM
 FILE REFERENCE: 058711
 CURRENT APPLICATION NUMBER: US/10/000, 066
 CURRENT FILING DATE: 2001-12-04
 PRIORITY NUMBER: 091529, 064
 PRIOR FILING DATE: 1997-10-05
 PRIORITY NUMBER: HEI-9-274673
 PRIOR FILING DATE: 1997-10-07
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 160
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-000-066-1

Query Match 12.3%; Score 106; DB 12; Length 160;
 Best Local Similarity 26.3%; Pred. No. 0.0044; Indels 24; Mismatches 61; Gaps 5;
 Matches 36; Conservative 24; Gaps 5;

QY 33 CSDSGGLEVLYQSQDPLQ-DFGSVKEKCSQQLSINIRFGILREDIKEFLDIALMSMSG 91
 Db 25 CNSDDATISYSYCDHLKFPISIISSEPCIRLKGTFVHVERPFRGNLYKLYNLFI--- 80

QY 92 SVLNFSVP---ICEALPKKSFCGRRKGEOIYVAGPVNPEFTIPQGEYQVLILEY- 145
 Db 81 -SVNSIELPKRKVEVTLCHFDDDSVCRALKGETNTSIPFSPEGILPKGHRYCVAIA 139

QY 146 --TEKRSTVACANATI 160
 Db 140 GDTEEK-LFCLNFTI 154

RESULT 9

US-09-372-348-23
 Sequence 23 Application US/09372348A
 Publication No. US20030028005A1
 GENERAL INFORMATION:
 APPLICANT: Hedrick, Joseph A.
 APPLICANT: Wang, Lujuan
 APPLICANT: Zlotnik, Albert
 APPLICANT: Murgolo, Nicholas J.
 APPLICANT: Johnston, Jonathan R.
 APPLICANT: Greene, Jonathan A.
 APPLICANT: Johnston, James A.
 APPLICANT: Baan, J. Fernando
 TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
 FILE REFERENCE: DX0984X(2d)
 CURRENT APPLICATION NUMBER: US/09/372,348A
 CURRENT FILING DATE: 1999-08-11
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 23
 LENGTH: 160
 TYPE: PRT
 ORGANISM: primate
 US-09-372-348-23

Query Match 11.8%; Score 101.5; DB 12; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0015; Indels 11; Gaps 3;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 FTATLFLWLIIFPSCGGGGKAWPAFWCSDSGLEVLYQSQDPLQ-DFGSVKEKSQL 62
 Db 6 FFSFLF--SSIFT-----EAQKQWNCNSDASITYCDSKQYPISTINNPCTELK 55

QY 63 KSNINIRFGITLREDIKEFLDIALMSQGSSTVNFSPICERALPKSFPCGRRKGEIY 122
 Db 56 GSKLGLIHFYIPRDLKOLYKLYNLYITWTMNLPKRKEVICRGSDDDSYSPCRALKGETNT 115

QY 123 AGPVANPFTIPQGEYQVLILEY 143
 Db 116 TISFSFKGKFKFSKGKYKVWE 136

RESULT 10

US-10-000-066-7
 Sequence 7 Application US/10000066
 Publication No. US20020086364A1
 GENERAL INFORMATION:
 APPLICANT: HONJO, TASUKU
 APPLICANT: KATO, KEIZO
 APPLICANT: TADA, HIDENAKI
 TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM
 FILE REFERENCE: 058711
 CURRENT APPLICATION NUMBER: US/10/000, 066
 CURRENT FILING DATE: 2001-12-04
 PRIORITY NUMBER: 091529, 064
 PRIOR FILING DATE: 1997-10-07
 PRIORITY NUMBER: HEI-9-274673
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 160
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-000-066-7

Query Match 11.8%; Score 101.5; DB 12; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0.0015; Indels 11; Gaps 3;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;

QY 4 FTATLFLWLIIFPSCGGGGKAWPAFWCSDSGLEVLYQSQDPLQ-DFGSVKEKSQL 62
 Db 6 FFSFLF--SSIFT-----EAQKQWNCNSDASITYCDSKQYPISTINNPCTELK 55

QY 63 KSNINIRFGITLREDIKEFLDIALMSQGSSTVNFSPICERALPKSFPCGRRKGEIY 122
 Db 56 GSKLGLIHFYIPRDLKOLYKLYNLYITWTMNLPKRKEVICRGSDDDSYSPCRALKGETNT 115

QY 123 AGPVANPFTIPQGEYQVLILEY 143
 Db 116 TISFSFKGKFKFSKGKYKVWE 136

RESULT 11

US-09-372-348-26
 Sequence 26 Application US/09372348A
 Publication No. US20030028005A1
 GENERAL INFORMATION:
 APPLICANT: Hedrick, Joseph A.
 APPLICANT: Wang, Lujuan
 APPLICANT: Zlotnik, Albert
 APPLICANT: Murgolo, Nicholas J.
 APPLICANT: Greene, Jonathan R.
 APPLICANT: Johnston, James A.
 TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods

```

; FILE REFERENCE: DX0884K(2d)
; CURRENT APPLICATION NUMBER: US/09/372,348A
; CURRENT FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 26
; LENGTH: 141
; TYPE: PRT
; ORGANISM: primate
; US-09-372-348-26

Query Match 11.2%; Score 96.5; DB 10; Length 141;
Best Local Similarity 25.6%; Pred. No. 0.0049; Mismatches 56; Indels 11; Gaps 3;
Matches 30; Conservative 20; Mismatches 56; Indels 11; Gaps 3;

RESULT 12
US-09-899-917-17
Sequence 17, Application US/09899917
Patent No. US2002011952A1
GENERAL INFORMATION
APPLICANT: Olsen, Henrik S.

TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,917
FILING DATE: 09-JUL-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 03/994,962
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:
NAME Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0440002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. US2002011952A1 Relevant
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-899-917-17

Query Match 10.9%; Score 94; DB 9; Length 60;
Best Local Similarity 33.3%; Pred. No. 0.003;

; Query Match 11.2%; Score 96.5; DB 10; Length 141;
; Best Local Similarity 25.6%; Pred. No. 0.0049; Mismatches 56; Indels 11; Gaps 3;
; Matches 30; Conservative 20; Mismatches 56; Indels 11; Gaps 3;

Query Match 9.5%; Score 81.5; DB 12; Length 555;
Best Local Similarity 25.7%; Pred. No. 1.9; Mismatches 32; Indels 25; Gaps 4;
Matches 26; Conservative 18; Mismatches 32; Indels 25; Gaps 4;

RESULT 13
US-10-424-599-214951
Sequence 214951, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovacic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 214951
LENGTH: 555

TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(555)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE: unsure
OTHER INFORMATION: Clone ID: PAT_MRT847_36126C.1.pep
US-10-424-599-214951

Query Match 9.5%; Score 81.5; DB 12; Length 555;
Best Local Similarity 25.7%; Pred. No. 1.9; Mismatches 32; Indels 25; Gaps 4;
Matches 26; Conservative 18; Mismatches 32; Indels 25; Gaps 4;

RESULT 14
US-10-424-599-199134
Sequence 199134, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovacic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO: 199134
LENGTH: 170
TYPE: PRT

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ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21842C.1.pep
US-10-424-599-199134

Query Match 9.4%; Score 81; DB 12; Length 170;
Best Local Similarity 21.1%; Pred. No. 0.43; Mismatches 59; Indels 52; Gaps 7;
Matches 35; Conservative 20; Mismatches 59; Indels 52; Gaps 7;

Qy 24 GAK-PTHVCSDS---GLEVLYQSCBLOPGRFSVEK----- 57
Db 23 GASWVPOVTVKERYKVGRDNPLYFCADP-ADYLQIHKVDLDPNPPKPKGEKLAKASGD 81

Qy 58 - --CSKQJKSNINRFGILREDIKEFLDIALMSQGSSVLANFSYVIFCEAALPKSFCCGRKGQIY 113
Db 82 FKEEVGEGSKHMGKVGLI-----TLINOERDADCTIEQADLKCP 122

Qy 114 RKGBQIYVAGPVNNEFTIPQGVQVLLVLYEKRSTVACANATI 159
Db 123 LKKGB-LSUTKDVSLPR-BIPGSIYVLADEVYEDGKTCUTAKI 166

RESULT 15
US-10-282-122A-7726
; Sequence 77326, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hasselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: BLTRA-034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 6/0191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 6/0206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 6/0207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 6/0230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 6/0230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 6/0242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 6/0253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 6/0257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 6/0267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 6/0269,308

PRIOR FILING DATE: 2001-03-16

Remaining Prior Application data removed - See File wrapper or PALM.

NUMBER OF SEQ ID NOS: 7864

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 77326

LENGTH: 876

TYPE: PRT

ORGANISM: Vibrio cholerae

9.0%; Score 78; DB 12; Length 876;

US-10-282-122A-77326

Query Match

| | | | | |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|--------------|-------|---------------------------|
| Copyright (c) 1993 - 2004 Compugen Ltd. | GenCore version 5.1.6 | | | |
| OM protein - protein search, using sw model | | | | |
| Run on: | April 29, 2004, 15:21:06 ; Search time 21 seconds | | | |
| Title: | US-09-899-917-2 | | | |
| Perfect score: | 862 | | | |
| Sequence: | I MKGFTATIPLWTLIFPSGSG.....ELYTERKSTVACANATIMCS 162 | | | |
| Scoring table: | BLOSUM62 | | | |
| Gapop 10.0 , Capext 0.5 | | | | |
| Searched: | 283366 seqs, 96191526 residues | | | |
| Total number of hits satisfying chosen parameters: | 283366 | | | |
| Minimum DB seq length: 0 | | | | |
| Maximum DB seq length: 200000000 | | | | |
| Post-processing: | Minimum Match 0%
Maximum Match 100% | | | |
| Listing first 45 summaries | | | | |
| Database : | PIR_78:* | | | |
| 1: pir1:* | | | | |
| 2: pir2:* | | | | |
| 3: pir3:* | | | | |
| 4: pir4:* | | | | |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution, | | | | |
| SUMMARIES | | | | |
| Result No. | Score | Query Length | DB ID | Description |
| 1 | 344 | 39.9 | 160 | 2 S11633 |
| 2 | 344 | 39.9 | 160 | 2 S11633 |
| 3 | 81 | 9.4 | 406 | 2 H71139 |
| 4 | 79.9 | 9.2 | 484 | 2 H8423 |
| 5 | 78 | 9.0 | 1133 | 2 S55496 |
| 6 | 77.5 | 9.0 | 394 | 2 A75012 |
| 7 | 77.5 | 9.0 | 428 | 2 T15259 |
| 8 | 77 | 8.9 | 246 | 2 AH0393 |
| 9 | 77 | 8.9 | 739 | 2 G96740 |
| 10 | 76.5 | 8.9 | 294 | 2 T22158 |
| 11 | 76.5 | 8.9 | 436 | 2 T28066 |
| 12 | 76.5 | 8.9 | 452 | 1 VGBG3 |
| 13 | 76.5 | 8.9 | 471 | 2 E86192 |
| 14 | 75.5 | 8.8 | 342 | 2 D88308 |
| 15 | 75.5 | 8.8 | 1215 | 2 C84846 |
| 16 | 75.5 | 8.8 | 1241 | 2 F97286 |
| 17 | 75 | 8.7 | 699 | 2 A96529 |
| 18 | 74.5 | 8.6 | 484 | 2 T16695 |
| 19 | 74.5 | 8.6 | 442 | 1 VGBEA |
| 20 | 73.5 | 8.5 | 481 | 2 B97348 |
| 21 | 73 | 8.5 | 1106 | 2 A97919 |
| 22 | 72 | 8.4 | 409 | 2 E90299 |
| 23 | 72 | 8.4 | 686 | 1 D70172 |
| 24 | 72 | 8.4 | 1218 | 2 S71376 |
| 25 | 72 | 8.3 | 267 | 2 B90866 |
| 26 | 71.5 | 8.3 | 1513 | 1 RNR022 |
| 27 | 71.5 | 8.3 | 1 | Nature 402, 761-768, 1999 |
| 28 | 71 | 8.2 | 668 | 2 S556909 |
| 29 | 71 | 8.2 | 2 | T01103 |

A; Reference number: A84420; MUID:20083487; PMID:10617197
 A; Accession: G84581
 A; Status: Preliminary
 A; Molecule type: DNA

A; Residues: 1-1137 <STO>

A; Cross-references: GB:AE002093; NID:93687234; PIDN: AAC62132.1; GSPDB:GN00139

C; Genetics:

A; Gene: At2g19840

A; Map position: 2

Query Match 11.5%; Score 99; DB 2; Length 1137;

Best Local Similarity 26.3%; Pred. No. 0_13; Mismatches 23; Indels 42; Gaps 7; Matches 36; Conservative 23; Mismatches 42; Indels 36; Gaps 7;

Qy 10 LWTMILFPPSGG-----GGGGKAWPHTWVCSDSLGEVLYQSCDPLQDFGFVY-- 55
 Db 448 LWTMSAVPPTPSGLKRGFCVWVYQSGEKDPR---AKKGVFGFY---PNWGKGRVMMI 499

Qy 56 -EKCSKQLKSNINIRFG----LREDIKEFLDIALMSQSSVUNPSYPICEAALPKPSFCG 113
 Db 500 BEERCS-----ISRNWVFREDV--MKD--ILNOSTSGMSDFDLATRNPSPCAG 547

Qy 114 RSKEQQIVYAGPVNNPE 130
 Db 548 NRKEDEISVQGVNSDDD 564

RESULT 3
 H71139

hypothetical protein PH0331 - Pyrococcus horikoshii

C; Species: Pyrococcus horikoshii

C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000

C; Accession: H71139
 R; Kawarabayashi, Y.; Savada, M.; Horikawa, H.; Haikawa, Y.; Hiro, Y.; Yamamoto, S.; Sakit M.; Ohfuki, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kubida, N.; Oguchi DNA. Res. 5, 55-76, 1998

A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A; Reference number: A71000; MUID:98344137; PMID:9679194

A; Accession: H71139

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-406 <KAW>

A; Cross-references: GB:AP000002; NID:93236129; PIDN:BA229405.1; PID:93256722

A; Experimental source: Strain OT3

A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:

A; Gene: PH0331

C; Superfamily: conserved hypothetical protein PAB127

Query Match 9.4%; Score 81; DB 2; Length 406;

Best Local Similarity 25.8%; Pred. No. 2_6; Mismatches 39; Conservative 27; Mismatches 49; Indels 36; Gaps 9; Matches 406;

Qy 1 MKG--PTATLFLWTFPSGGGGKA-WPPTHVCSDSLGEVLYQSCDPLQDFGF--SV 55
 Db 4 MKGASFVFTFLWTFVMSLIFGPGKLAVALPFLLLI--MGLLF--DAPGDFEVERI 56

Qy 56 EKC---SKQLKSNINIRFG---LREDIKEFLDIALMSQSSVUNPSYPICEAAL 106
 Db 57 EKAGTQFVGNEEVLYVRVERGIGLVMNRENTIPRAF---MTSSGSNVGYF----- 103

Qy 107 PKFSFGGRKKEQIYAGPVNNPEFTIPOGEE 137
 Db 104 --FTPGRGRSPQPSVSKLPKRGVVEIPIKME 132

RESULT 4
 H84723

probable triacylglycerol lipase [imported] - Arabidopsis thaliana (mouse-ear cress)

C; Species: Arabidopsis thaliana (mouse-ear cress)

C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 /

C; Accession: H84723
 R; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, I.; Tallon, L.

euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the Plant Arabidopsis thaliana.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: H84723

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-484 <STO>

A; Cross-references: GB:AE002093; NID:94582461; PIDN:AAD24845.1; GSPDB:GN00139

C; Genetics:

A; Gene: At2g1690

A; Map position: 2

Query Match 9.2%; Score 79.5; DB 2; Length 484;

Best Local Similarity 27.4%; Pred. No. 4_6; Mismatches 43; Indels 29; Gaps 5; Matches 34; Conservative 18; Mismatches 43; Indels 29; Gaps 5;

Qy 35 DSGLEVLYSCDPLQDFGFG3SVEKSKQLKSNINIRFGTLREDIKEFLDIALMSQSSV 94
 Db 248 ESGFLSILVYSDESKSFG--LESQRQQLSEIS--RIMNKVGEENMSITLGHSMSSL 302

Qy 95 LN-FSYPICTAAALPK-----FSPGRRKGE-----QIYVAGPVNNPE 130
 Db 303 AQLAYDIAEGLGNRNRIGKDIPTVFSHAGPVRGVNLSEKKRCBEGLVKVLRTINVDPV 362

Qy 131 FTIP 134
 Db 363 TKLP 366

RESULT 5
 B82163

DNA topoisomerase I VC730 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C; Species: Vibrio cholerae

C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C; Accession: B82163

R; Heidelberg, J.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chardron, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

1, R.R.; Makalanski, J.J.; Ventler, J.C.; Fraser, C.M.

Nature 405, 477-483, 2000

A; Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A; Reference number: A82035; MUID:20406833; PMID:10952301

A; Accession: B82163

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-876 <HEI>

A; Cross-references: GB:AB004251; GB:AB003852; NID:96556248; PIDN:AAF94880.1; GSPDB:GN001;

A; Experimental source: Berogroup 01; strain N16961; biotype El Tor

C; Genetics:

A; Gene: VC1730

A; Map position: 1

C; Superfamily: bacterial type I DNA topoisomerase

Query Match 9.0%; Score 78; DB 2; Length 876;

Best Local Similarity 26.1%; Pred. No. 13; Mismatches 40; Indels 42; Gaps 10; Matches 37; Conservative 23; Mismatches 40; Indels 42; Gaps 10;

Qy 8 LEWTFLWTFPSGGGGKA-WPPTHVCSDSLGEVLYQSCDPLQDFGFVYKCSKQLK 65
 Db 599 IWTNTLICPTCSRPMGIRTASTGVFLGPGCGVYGLP-----PKERC---KTT 640

Qy 66 INT--RAGL--LREDIKEFLDIALMSQSSVUNPSYPICEAALPKFRCGRKRGKQTY 121
 Db 641 INGDDEGVINLEBEY---TAALRAKRC----PCETANDLDDKRC--IH 687

Qy 122 YAGPVNNPE--FTPQGEYQV 140
 Db 688 VCG--NNPNCBGFIVEEGEPKV 707

RESULT 6
 S54496

probable membrane protein YPR022c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein Ypr9367.02c

C;Species: *Saccharomyces cerevisiae*

C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002

T14529
R;Beddoe, K.; Churcher, C.M.

submitted to the EMBL Data Library, May 1995

A;Accession: S54495

A;Molecule type: DNA

A;Cross-references: EMBL:Z49274; NID:9809585; PID:9809587; GSPDB:GN0016; MIPS:YPR022c

A;Experimental source: strain AB972

A;Genetics:

A;Gene: MIPS:YPR022c

A;Cross-references: SGD:S0006226

A;Map position: 16R

C;Keywords: transmembrane protein

F;52-54/Domain: transmembrane #status predicted <TM1>

F;68-784/Domain: transmembrane #status predicted <TM2>

F;931-947/Domain: transmembrane #status predicted <TM3>

F;971-987/Domain: transmembrane #status predicted <TM4>

Query Match 9.0%; Score 78; DB 2; Length 1133;

Best Local Similarity 25.3%; Pred. No. 17; Mismatches 31; Indels 62; Gaps 8;

Matches 37; Conservative 16; Mismatches 31; Indels 62; Gaps 8;

QY 46 DPLQPGFSVKECS-----KQLKS--NINTRFGIT---LREDTKE 80

472 DPLTKVSKERKQCQENFSFVPELRVSVIESIHKSLKSFWLNPHQYGLHKSFRHDKP 531

QY 81 LFLDAIMSGQSIVNSFY----PICEALPKSFCCRGQIYVAGPV----NRP 129

Db 532 AILNLALIMTCASAFGSEYRQQSDIC-----GPLRWTIFSA 570

QY 130 EFTIPOCBYQV---LLELYTEKRST 151

Db 571 DFPQPSKTYIIOQSLLIVLEGY-EKTST 595

Db 571 DFPQPSKTYIIOQSLLIVLEGY-EKTST 595

RESULT 7

A75012
conserved hypothetical protein PAB1277 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000

C;Accession: A75012

R;anonymous. Genoscope

submitted to the EMBL Data Library, July 1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Accession: A75012

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-334 <KRW>

A;Cross-references: GB:AJ428288; GB:AL096836; NID:95458960; PIDN:CAB50535.1; PID:9545904

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB1277

C;Superfamily: conserved hypothetical protein PAB1277

Query Match 9.0%; Score 77.5; DB 2; Length 394;

Best Local Similarity 23.4%; Pred. No. 5; Mismatches 31; Indels 44; Gaps 9;

Matches 36; Conservative 31; Mismatches 44; Indels 43; Gaps 9;

QY 1 MKG---FTATIPLFTLIPSCS3GGGKA-WPTHWVCSDSGLVFLVYQSCDPLQDFGSVEK 57

1 MGRGVSFPLTFMLFVLSVIFGTPGKALFPMLII---WQMIFDT---PGGTVER 51

QY 58 -----CSQIKSNNTIRG----ILRDIKEFLDLAAMSQSSVAN-FSPICE 103

52 EVTRGRVFGVGEVKLVRVSKIGVIGVTKMLPRAF----EVKSATRFFTPGKR 106

QY 104 ALPKFKSPGCRKQEIQIVYAGPVVNPEFTIPOQCR 137

Db 107 EFSFSEFSVPRKG-----EYDIPKTE 128

T14529
S;locus-specific glycoprotein - wild cabbage (fragment)

N;Alternate names: S glycoprotein

C;Species: Brassica oleracea (wild cabbage)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000

C;Accession: T14529

R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.

Proc. Natl. Acad. Sci. U.S.A. 94: 7673-7678, 1997

A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class

echanism.

A;Reference number: Z18078; MUID:97352858; PMID:9207151

A;Accession: T14529

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Residue: 1-428 <KTS>

A;Cross-references: EMBL:D85205; NID:g2351141; PIDN:BA21939.1; PID:92351142

C;Superfamily: S-loctus-specific glycoprotein; S-loctus-specific glycoprotein homology

C;Keywords: Glycoprotein

Query Match 9.0%; Score 77.5; DB 2; Length 429;

Best Local Similarity 25.2%; Pred. No. 6; Mismatches 27; Indels 20; Gaps 4;

Matches 27; Conservative 20; Mismatches 49; Indels 11; Gaps 4;

QY 49 QDGFPSVKEKSQLKSINTNRFGITREDIKEFLDLAAMSQSSVANPIPCALPK 106

Db 149 QSDFDPPTDILPFLEMKLYNKLKGU---NRFLTAWSRSDPPSGDVSQKLENRELPE 201

QY 109 FSPGGRKKEQDPIYAGPVNPNPFT-IPOGE-YQVLLYTRKRTVA 153

Db 202 FYLU-LKGFOVERSGPWNNGVRPSGIPENQKLSIMVWNPTESEVA 246

RESLT 9

AH0393
probable exported protein YPO3241 [imported] - *Yersinia pestis* (strain CO92)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C;Accession: AH0393

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;

de Jong, M.; Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hance, A.; Harris, D.; Hatcher, J.; Hinton, J.; Hogg, C.; Impey, D.; James, K.; Johnson, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.I.; Nature, 413, 523-527, 2001

A;Title: Genome Sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0393

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-246 <KUR>

A;Cross-references: GB:AL530842; PIDN:CA92476.1; PID:915981177; GSPDB:GN00175

C;Genetics:

A;Gene: YPO3241

C;Superfamily: Escherichia coli probable membrane protein yafK

Query Match 8.9%; Score 77; DB 2; Length 246;

Best Local Similarity 29.0%; Pred. No. 3; Mismatches 31; Indels 34; Gaps 6;

Matches 31; Conservative 12; Mismatches 30; Indels 34; Gaps 6;

QY 45 CDPLQDFGFSVKECQLSKNTIIRFGITREDIKEFLDLAAMSQSSVAN 98

Db 13 CLPAASFTFSRSEAVAKSLKQOLQGSSVVIQKFERRVLEYAKL---QGEYRQVS 68

Query Match 8.9%; Score 77; DB 2; Length 394;

Best Local Similarity 23.4%; Pred. No. 5; Mismatches 31; Indels 44; Gaps 9;

Matches 36; Conservative 31; Mismatches 44; Indels 43; Gaps 9;

QY 99 YPICEALPKSFCCG----RRKGEOQIVYAGPVNPNPFTIPOQCR 140

Db 69 YPICE-----FSGGLGPKREG-----DFKSPGFIYI 96

RESLT 10

G96740

C;Genetics:
A;Gene: 72
C;superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
F;1-19;/Domain: signal sequence #status predicted <SIG>
F;20-452;/Domain: hydrophobic <HYB>
F;404-422;/Domain: transmembrane #status predicted <TM2>
F;403,111,347,396;/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;347,396;/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.9%; Score 76.5; DB 1; Length 452;
Best Local Similarity 26.0%; Pred. No. 8; 5; Mismatches 44; Conservative 16; Indels 47; Gaps 8;
Matches 44; Mismatches 62; Indels 47; Gaps 8;

Qy 2 KGFATIPLFLWILIFPSCSGGGGKAWPHTWVCSDSGLEVIQSOPCDPLDFGSVEKCSKQ 61
Db 161 KTYSARL-TWPKIMPIC-----APPIH-----DYSYMKNPKLSPAMCDE---- 199

Qy 62 IKSNTINIRFGITI-LRDEIKFLFLDIALMWSQGSSV-----NFSYSPICEAA 105
Db 200 -FSDILWQASLTMAATDDGLVILAPAHSAASGLYRRTVTDORRIYDFSVTIPSER 258

Qy 106 LP-----KFSFPCGRRKGEQIYAGPVNN-----PEFTIPCGEYQVILEY 145
Db 259 CPIAFEOCFGNDRCKIPEQIYSGREVFTRRLGEFPNFPQGEHMWTWKFW 307

RESULT 14
E86192 hypothetical protein [imported] - arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86192
R/Theologis, A.; Becker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creaby, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huijzer, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Duro, J.S.; Maiti, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Autors: Salzberg, S.L.; Schwartz, J.R.; Sinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86192
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-471 <STO>
A;Cross-references: GB:AB005172; NID:96850308; PIDN:AAF29385.1; GSPDB:GN00141
A;Genetics:
A;Map Position: 1

Query Match 8.9%; Score 76.5; DB 2; Length 471;
Best Local Similarity 26.6%; Pred. No. 8; 9; Mismatches 33; Conservative 19; Indels 43; Gaps 29; Gaps 5;
Matches 33; Mismatches 43; Indels 29; Gaps 5;

Qy 35 DSGLEVLVQSCDPLQDFPSVKEKSKDKSNINIRFGITI-LRDEIKFLFLDIALMWSQGSSV 94
Db 237 ESCPGLGLTSGESSESKFG--LSECREQJLSEIS--RIMNKHKGEEISITLGHSMSSL 291

Qy 95 LN PSYPCLEARPK-----SFPCGRRKGE-----QIVYAGPVNNPE 130
Db 292 AQQLAYDIAELGMNQRDRKEPKPVPTVFSFAGPRVGNLGFKCRCEELGVVKVLRITVNNDPI 351

Qy 131 FTIP 134
Db 352 TKLP 355

RESULT 15
DB1306 probable UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecapeptide

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: April 29, 2004, 15:21:06 ; Search time 17 Seconds
 (without alignments)
 495.198 Million cell updates/sec

Title: US-09-899-917-2

Perfect score: 862

Sequence: 1 MKGFTATIFLMLLIFPSCSG.....LYTEKRSTVACANATIMCS 162

Scoring table: BLOSUM62
 Gappen 10 0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID Description

1 862 100.0 162 1 LY86_HUMAN

2 613 71.1 1 LY86_MOUSE

3 336 39.0 1 LY86_CHICK

4 125 14.5 1 LY86_BOVIN

5 124 14.5 1 LY86_CRIGR

6 106 12.3 1 LY86_MOUSE

7 101.5 11.8 1 LY86_HUMAN

8 78 9.0 1 T021_VIBCH

9 77 8.9 1 CYSC_VIBVA

10 77 8.9 1 CYSC_VIBVU

11 76.5 8.9 1 VGD_HSEVA

12 76.5 8.9 1 VGD_HSEVB

13 75.5 8.8 1 MURG_CANJE

14 75.5 8.8 1 RODP_CLOAB

15 75 8.7 1 JAK1_HUMAN

16 73.5 8.5 1 VGD_HSEVK

17 73.5 8.5 1 GATA_THETN

18 72.5 8.4 1 IBB6_HUMAN

19 72 8.4 1 REEG_BOBNU

20 71.5 8.3 1 RODP_EUGVTA

21 71 8.3 1 RODP_ORYVA

22 71 8.2 1 PBD2_YEAST

23 70.5 8.2 1 CAK2_ARATH

24 70.5 8.1 1 CYSC_VIBCH

25 70 8.1 1 RODP_BACUD

26 70 8.1 1 ATC1_YEAST

27 69.5 8.1 1 SDD2_SALTI

28 69.5 8.1 1 SDD2_SALTY

29 69 8.0 1 NICA_MOUSE

30 69 8.0 1 RIA2_CWNCB

31 68.5 7.9 200 1 RUVKA_STAM

32 68.5 7.9 474 1 PPAR_TWOB

33 68.5 7.9 1616 1 RRP2_TWOB

| RESULT | 1 | LY86_HUMAN | STANDARD; | PRT: | 162 AA. |
|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------|-----------|------|---------|
| ID | LY86_HUMAN | | | | |
| AC | Q9T7I1; Q9UQC4; | | | | |
| DT | 28-FEB-2003 (Rel. 41, Created) | | | | |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | | |
| DB | Lymphocyte antigen 86 precursor (MD-1 protein). | | | | |
| GN | LY86 OR MD1. | | | | |
| OS | Homo sapiens (Human) | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OC | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=retal liver, and Spleen; | | | | |
| RX | MEDLINE-99180501; PubMed=1079183; | | | | |
| RA | Miura Y., Shimazu R., Miyake K., Akashi S., Ogata H., Yamashita Y., Narisawa Y., Kimoto M., | "RP105 is associated with MD-1 and transmits an activation signal in human B cells.", | | | |
| RL | RJ:2815-2822(1998). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE OF 45-162 FROM N.A. | | | | |
| RC | TISSUE=monocytes; | | | | |
| RA | MEDLINE-99180501; PubMed=1079183; | | | | |
| RA | Begum N.A., Tsuji S., Nomura M., Shida K., Azuma I., Hayashi A., Matsubumi M., Sera T., Toyoshima K., | "Human MD-1 homologue is a BCG-regulated gene product in monocytes: its identification by differential display." | | | |
| RT | Hirokawa Y., Shimizu T., | | | | |
| RL | Biochem. Biophys. Res. Commun. 256:325-329(1999). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=retal liver, and Spleen; | | | | |
| RA | Williams S.; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=retal liver, | | | | |
| RA | MEDLINE-22380257; PubMed=12477932; | | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B.R., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hiech F., Diatchenko L., Matsunaga A., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohmyuki S., Carninci P., Prange C., Raha S.S., Loqueline N.A., Peters J., Abramson R.D., Mullany S.J., Boksa S.A., McLean P.J., McFernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W., Villalon D.K., Munro D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E., Schmerl A., Schein J.E., Jones S.J.M., Marr M.A., | | | | |
| RN | [5] | | | | |

Grand finale

P27822 oryctolagus
 Q02790 homo sapien
 Q8cgf6 rattus norvegicus
 Q09092 brassica oleracea
 Q8c990 staphylococcus
 Q971z5 sulfuroloous
 Q58027 methanococcus
 P27124 myctoclagus
 P26562 influenza a
 P04104 mus musculus
 Q98935 gallus gallus
 Q00706 emericella

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RT R.L.
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16199-16902 (2002).
 -i- FUNCTION: May cooperate with CD180 and TIR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS) and cytokine production. Important for efficient CD180 cell surface expression (By similarity).

-i- SUBUNIT: Binds CD180.

-i- SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the cell surface.

-i- TISSUE SPECIFICITY: Highly expressed in B-cells, monocytes and tonsil.

-i- INDUCTION: In monocytes down-regulated by the cell-wall fraction of Mycobacterium bovis (BCG-CWBS).

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CC EMBL; AF057178; AAC98152.2; -; ALT_INIT.

CC DR EMBL; AB020499; BAA7610.1; ALT_INIT.

CC DR EMBL; AL031123; CAB76262.1; -.

CC DR EMBL; BC03846; AAH38846.1; -.

CC DR Genew; HGNC:16837; LY86.

CC DR MIM; 605241; -.

CC DR GO:0005886; C:plasma membrane; TAS.

CC DR GO; GO:000915; P:apoptosis; TAS.

CC DR GO; GO:0008233; P:cell proliferation; TAS.

CC DR GO; GO:00059; P:humoral immune response; TAS.

CC DR InterPro; IPR003172; El_DerP2_DerP2.

CC DR InterPro; IPR007110; Ig-like.

CC DR Pfam; PF02221; El_DerP2_DerP2; 1.

CC DR SMART; SM0737; ML; 1.

CC DR SIGNAL 1 20 Immune response; Inflammatory response; Signal; Polymorphism.

FT CHAIN 21 162 LYMPHOCYTE ANTIGEN 86 (POTENTIAL).

FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).

FT VARIANT 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).

FT 160 160 M-> V (in QDSNP:1802323).

FT SEQUENCE 162 AA; 11905 MW; JEB6497E2DB4C6F27 CRC64;

Query Match 100.0%; Score 862; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 2e-82; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

RESULT 2 LY86_MOUSE STANDARD PRT; 162 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_MOUSE STANDARD PRT; 162 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; OC OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TAXID=109090; RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 20-44. RC TISSUE=B-cell; RX MEDLINE:9834386; PubMed=986597; RA Miyake K., Shimazu R., Kondo J., Niki T., Akashi S., Ogata H., RA Yamashita Y., Miura Y., Kimoto M.; "Mouse MD-1, a molecule that is physically associated with RP105 and positively regulates its expression.", J. Immunol. 161:1348-1353 (1998). RL [2] FUNCTION. RX MEDLINE:20384784; PubMed=10925274; RA Gorczyński R.N., Chen Z., Clark D.A., Hu J., Yu G., Li X., Tsang W., RA Haddad S.; "Regulation of gene expression of murine MD-1 regulates subsequent T cell activation and cytokine production.", J. Immunol. 165:1225-1332 (2000). RL -i- SUBCELLULAR LOCATION: Binds CD180. CC -i- FUNCTION: May cooperate with CD180 and TIR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS) and cytokine production. Important for efficient CD180 cell surface expression. CC -i- SUBCELLULAR LOCATION: Extracellular; associated with CD180 at the cell surface. CC -i- TISSUE SPECIFICITY: Highly expressed in spleen, liver, brain and thymus, and at lower levels in kidney. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AB007599; BA32399.1; -.

CC DR MGD; MGI:1321404; LY86.

CC DR InterPro; IPR003172; El_DerP2_DerP2.

CC DR InterPro; IPR007110; Ig-like.

CC DR Pfam; PF02221; El_DerP2_DerP2; 1.

CC DR SMART; SM0737; ML; 1.

CC DR SIGNAL 1 19 Immune response; Inflammatory response; Signal.

FT CHAIN 20 162 LYMPHOCYTE ANTIGEN 86 (POTENTIAL).

FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).

FT SEQUENCE 162 AA; 17811 MW; EED25DBE649372B CRC94;

Query Match 71.1%; Score 613; DB 1; Length 162; Best Local Similarity 66.7%; Pred. No. 1.5e-56; Matches 108; Conservative 22; Mismatches 32; Indels 0; Gaps 0; Gaps 0;

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

RESULT 3 LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

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 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120

Qy 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162
 Db 121 YAGPVNNEFTIPOGEYVQLELYTEKSTVACANATMCS 162

LY86_CHICK STANDARD PRT; 160 AA.

Qy 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60
 Db 1 MKGFTATILWLTIPSCGGGGKAMPHVYVSDSLEVLVOSCDPLQDFGSVERCSK 60

Qy 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI 120
 Db 61 OLKSNNIRPGIILREDIKEFLDIALMSQSSVLFNSYPICRAALKFSFCRKGQI

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetellus;
 OC NCBI_TaxID:10029;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT TYR-95.
 RC TISSUE-Ovarian carcinoma;
 RX MEDLINE=21229172; PubMed=1435574;
 RA Schirom A.B., Lien E., Henneke P., Chow J.C., Yoshimura A., Heine H.,
 RA Latz E., Monks B.G., Schwartz D.A., Miyake K., Goenbock D.T.;
 RT Molecular Genetic analysis of an endotoxin nonresponder mutant cell
 RT line. A point mutation in a conserved region of MD-2 abolishes
 RT endotoxin-induced signaling.";
 RL J. Exp. Med. 194:79-88(2001).
 CC -!- FUNCTION: Cooperates with TLR4 in the innate immune response to
 bacterial lipopolysaccharide (LPS), and with TLR2 in the response
 to cell wall components from Gram-positive and Gram-negative
 bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells
 expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS
 (BY similarity).
 CC -!- SUBUNIT: Heterogeneous homopolymer formed from homodimers;
 CC disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96
 CC and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (BY
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF325501; AAC57984.1; -.
 DR InterPro; IPR003172; El_DerP2-DerF2.
 DR InterPro; IPR007110; Ig-like_Pfam; PF02221; El_DerP2-DerF2; 1.
 DR SMART; SM00737; Mj_1.
 KW Immune response; Inflammatory response; Signal; Glycoprotein;
 KW Polymorphism.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 160 LYMPHOCYTE ANTIGEN 96.
 FT DISULFID 95 105 BY SIMILARITY.
 FT CARBOHYD 26 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 95 95 C->Y (IN ENDOTOXIN NONRESPONDER).
 SQ SEQUENCE 160 AA;
 18357 MW; 0B53B1A5B46DD6 CRC64;
 Query Match 14.4%; Score 124; DB 1; Length 160;
 Best Local Similarity 25.4%; Pred. No. 1e-05; Mismatches 33; Conservative 23; Mismatches 72; Indels 2; Gaps 2;
 Matches 33;
 OY 33 CDSDELIVLVLQSCPLQ-DFGFSPEKCSQLKINIRGILIREDKELFLDIALMSQ 91
 OY |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 OY 25 CNSSATPSYSYCDSMKFFPSITABPCITIIGNGFLHFKFIRRDRDLYMISINNS 84
 OY 92 SSVLNFSYPTCCEALPKFSSGRRKGEQIYAGVNNPPEFTIQQEGYQVLL-LYTEKRS 150
 OY |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 OY 85 LEVPRKEKICHGDNYSICKALKGETWTVVPSKILFPGQXCVASAVGNEE 144
 OY |:|:|:|:|:|:|:|:|:|:|:
 OY 151 YVACANATIM 160
 OY 145 KLFCLNFTI 154
 RESULT 6
 LY96_MOUSE STANDARD; PRT; 160 AA.
 ID Q9JTF9;
 AC 09JTF9;
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Lymphocyte antigen 96 precursor (MD-2 protein) (ESOP-1).
 GN LY96 OR MD2 OR ESOP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mirinae; Mus;
 OC NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20352025; PubMed=10891475;
 RA Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.;
 RT "ESOP-1, a secreted protein expressed in the hematopoietic, nervous,
 and reproductive systems of embryonic and adult mice.";
 RL Blood 96:362-364(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-kidney;
 RX MEDLINE=2019199; PubMed=10725698;
 RA Akashi S., Shimada R., Ogata H., Nagai Y., Takeda K., Kimoto M.,
 Miyake K.;
 RA Arakawa T., Haro A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Irawa M., Nishi K., Kiyoeda H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saio R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann R., Gasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Masuo Y., Nikaido I., Pesce G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuto M., Hono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Rume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mahima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seja T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Wittkaker C., Wilming L.,
 RA Winstaw-Baris A., Yoshida K., Haegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashiizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:683-690(2001).
 CC
 CC -!- FUNCTION: Cooperates with TLR4 in the innate immune response to
 bacterial lipopolysaccharide (LPS), and with TLR2 in the response
 to cell wall components from Gram-positive and Gram-negative
 bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells
 expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS
 (BY similarity).
 CC -!- SUBUNIT: Heterogeneous homopolymer formed from homodimers;
 CC disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96
 CC and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (BY
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Highly expressed in spleen, bone marrow, levels
 CC thymus, liver, kidney, ovary and decidua. Detected at lower levels
 CC in testis, small intestine and skin.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF168120; AAF09634.1; -.

DR EMBL: AB018550; BAA93619.1; -.
 DR EMBL: AK019283; BAB31645.1; -.
 DR MGD; MGI:1341509; Ly6.
 DR InterPro; IPR003172; El_DerP2_DerF2.
 DR IparPro; IPR007110; Ig-like.
 DR Pfam; PF00221; El_DerP2_DerF2; 1.
 DR SMART; SM00737; ML; 1.
 DR Immune response; Inflammatory response; signal; glycoprotein.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 160 LYMPHOCTYE ANTIGEN 96.
 FT DISULFID 95 105 BY SIMILARITY.
 FT CARBOHYD 26 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 160 AA; 18394 MW; B224D1785D5429E2 CRC64;
 Query Match Local Similarity 12.3%; Score 106; DB 1; Length 160;
 Best Local Similarity 26.3%; Pid. No. 0.0076; DB 1; Length 160;
 Matcches 36; Conservative 24; Mismatches 61; Indels 16; Gaps 5;
 QY 33 CSDSGLEVKYQSCDPLQ-DGFSVKEKSKQLKSNINREGILLIREDIKEFLFDIALMSQ 91
 DB 25 CNSSDALTISYSYCDHLKFPISSSEP'CIRLJRTGNGFVHVFIPRNLKVLYNFI--- 80
 QY 92 SSVLNTSYP---ICEAALKFESCGRKKEQQIVYAGPNNPEPTIPQGEYQVILEY- 145
 Db 81 -SVNSTEBLPKRKEVLCHGDDDYSDSFCAKLGETVNTSIPSEFGILFPKHYRCVAATA 139
 QY 146 --TEKSTIVACNAMAT 160
 Db 140 GDTSEK--LFCINFTI 154

RESULT 7

| ID | HUMAN | STANDARD | PRT | 160 AA. |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|-----|---------------------------------------------|
| AC | 09Y679; | | | 28-FEB-2003 (Rel. 41, Last sequence update) |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) | | | |
| DE | Lymphocyte antigen 96 precursor (MD-2 protein) (ESOP-1). | | | |
| GN | LY96 OR MD-2 OR ESOP-1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxId=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-Uterus; | | | |
| RC | LINEAGE-9988036; PubMed=10359581; | | | |
| RA | Shimizu R., Akashi S., Ogata H., Nagai Y., Fukudome K., Miyake K., | | | |
| RA | Kimoto M.; "MD-2, a molecule that confers lipopolysaccharide responsiveness on Toll-like receptor 4," J. Exp. Med. 180:1777-1782(1999). | | | |
| RL | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=2035205; PubMed=10891475; | | | |
| RA | Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.; "Ly6, a secreted protein expressed in the hematopoietic, nervous, and reproductive systems of embryonic and adult mice," Blood 95:362-364(2000). | | | |
| RA | "A point mutation in a conserved region of MD-2 abolishes endotoxin-induced signaling," J. Exp. Med. 194:79-88(2001). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-95. | | | |
| RX | MEDLINE=21129172; PubMed=1143574; | | | |
| RA | Schliemann A.B., Liem E., Henneke P., Chow J.C., Yoshimura A., Heine H., Lutz B., Monks B.G., Schwartz D.A., Miyake K., Golenbock D.T.; "Molecular genetic analysis of an endotoxin nonresponder mutant cell line," J. Immunol. 171:61-66, LY96. | | | |
| RA | "M. endotoxin-induced signaling," J. Exp. Med. 194:79-88(2001). | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Liver; | | | |
| RX | MEDLINE=22388257; PubMed=12477932; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shearer C.M., Schulier G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., Blatchko L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Scarce M.B., Bonaldo M.F., Casavant T.L., Schetzen T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carnici U., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Milahy S.J., Basak S.A., McEwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farhey J., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.B., Jones S.J.M., Maira M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | |
| RN | [5] | | | |
| RP | INTERACTION WITH TLR2 AND TLR4. | | | |
| RX | MEDLINE=21103214; PubMed=11160242; | | | |
| RA | Dziarski R., Wang Q., Miyake K., Kirschning C.J., Gupta D.; "MD-2 enables Toll-like receptor 2 (TLR2)-mediated responses to lipopolysaccharides and enhances TLR2-mediated responses to Gram-positive and Gram-negative bacteria and their cell wall components," J. Immunol. 166:1938-1944(2001). | | | |
| RN | [6] | | | |
| RP | DISULFIDE-BONDS, AND CARBOHYDRATE-LINKAGE SITES. | | | |
| RX | MEDLINE=11593030; | | | |
| RA | Visintin A., Mazzoni A., Spitzer J.A., Segal D.M.; "Secreted MD-2 is a large polymeric protein that efficiently confers lipopolysaccharide sensitivity to Toll-like receptor 4," Proc. Natl. Acad. Sci. U.S.A. 98:12156-12161(2001). | | | |
| RN | [7] | | | |
| RP | INTERCHAIN DISULFIDE BOND. | | | |
| RX | MEDLINE=21477444; PubMed=1593030; | | | |
| RA | Mullen G.E.D., Kennedy M.N., Visintin A., Mazzoni A., Leifer C.A., Davies D.R., Segil D.M.; "The role of disulfide bonds in the assembly and function of MD-2," Proc. Natl. Acad. Sci. U.S.A. 100:919-924(2003). | | | |
| CC | -1 FUNCTION: Cooperates with TLR4 in the innate immune response to bacterial lipopolysaccharide (LPS), and with TLR2 in the response to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TIR-dependent activation of NF-kappa-B. Cells expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS. | | | |
| CC | -- SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4. | | | |
| CC | -- SUBCELLULAR LOCATION: Extracellular. | | | |
| CC | -- PTM: N-glycosylated; high-mannose. | | | |
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| CC | EMBL; AB018549; BAA78717.1; AM16821; AF089355.1; -. | | | |
| DR | EMBL; B0020650; ARB20590.1; -. | | | |
| DR | GeneDB; FGNC:17156; LY96. | | | |
| DR | MIM; 605243; -. | | | |
| DR | GO; GO:00150586; C:plasma membrane; TAS. | | | |
| DR | GO; GO:0015061; P:antibacterial humoral response (sensu Inver. . . ; TAS. | | | |

DR GO: GO:0007166; p:cell surface receptor linked signal transdu... : TAS.
 DR GO: GO:000968; p:cellular defense response; TAS.
 DR InterPro; IPR003172; E1_DerP2_DerF2.
 DR Pfam; PF0221; E1_DerP2_DerF2; 1.
 DR SMART; SM0037; M6; 1.
 KW Immune response; Inflammatory response; Signal; Glycoprotein.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 160 LYMPHOCYTE ANTIGEN 96.
 FT DISULFID 95 105
 FT CARBOHYD 26 25 N-LINKED (GlcNAc. .).
 FT CARBOHYD 114 114 N-LINKED (GlcNAc. .).
 FT MOTAGEN 95 105 C->Y: ABOLISHES LPS-RESPONSE.
 SQ SEQUENCE 160 AA; 18446 MW; 1E83A#P583636D7A CRG64;
 Query Match 11.8%; Score 101.5; DB 1; Length 160;
 Best Local Similarity 24.1%; Pred. No. 0 0022;
 Matches 34; Conservative 26; Mismatches 70; Indels 11; Gaps 3;
 Ov 4 FTAATLPLWLTIFRSCGGGGKAWPHTVCSGLEYVQSDPLO-DFGSVEKSQL 62
 Db 6 FSTILP--SSIFT----BAQKQFWCNNSDASISYTCQDKMQYPISVNNCIELK 55
 Ov 63 KSNINIRGIIREDIKEFLDIALMGSSTSINFSPYICBALPKPSFCRRKBOIYY 122
 Ov 56 GSKQLLHQYIPIRKDLYLIVNNTNNPFRKRVICRGSSDDISFCRAKGETVT 115
 Qy 123 AGGVNNPPTTIGGEYQVLE 143
 Db 116 TISFSFKGIKFSKGKYKCVVE 136

RESULT 8

TOP1_VIBCH STANDARD; PRT; 876 AA.
 AC QKRRB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE (Unwinding enzyme) (swivelase).
 GN topo OR vC1730.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR NI6961 / Serotype O1;
 RX MEDLINE=2040833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Embalava M.D., Vaishnavan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae." / Nature 406:477-483(2000).
 RT Nature 406:477-483(2000).
 CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the conversion of one topological isomer of DNA to another.
 CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA backbone bond, it simultaneously forms a protein-DNA link, in which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus at one end of the enzyme-severed DNA strand.
 CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase family.

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 CC -----
 DR EMBL; AM004251; AA#F94880.1; --.
 DR PIR; B8163; B82163.
 DR HSSP; P06612; IECL.
 DR TIGR; VC1730; --.
 DR InterPro; IPR00573; DNA_topI_bact.
 DR InterPro; IPR00330; DNA_topIsomerase.
 DR InterPro; IPR003611; DNAtopI_ATP_bind.
 DR InterPro; IPR003602; DNAtopI_DNA_bind.
 DR InterPro; IPR006117; Toprim_Dom.
 DR InterPro; IPR006154; Toprim_sub.
 DR Pfam; PF01331; Topoisom_bac; 1.
 DR Pfam; PF01751; Toprim_I.
 DR Pfam; PF01396; zf-C4_topoIom; 2.
 DR PRINTS; PR00117; PRTPISMWAREB1.
 DR SMART; SM00437; TOPIAC; 1.
 DR SMART; SM00436; TOPIBC; 1.
 DR TIGRFAMS; TIGR01051; topo_bact; 1.
 DR PROTEIN; TOPOISOMERASE_I_PROK; 1.
 DR Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
 KW Repeat; Complete proteome.
 FT ZN_FING 668 695 C4_TYPE 1.
 FT ZN_FING 717 742 C4_TYPE 2.
 FT ACT_SITE 327 327 DNA_CLEAVAGE (BY SIMILARITY).
 SQ SEQUENCE 876 AA; 97909 MW; 8A5BC0148CA1B753 CRG64;
 Query Match 9.0%; Score 78; DB 1; Length 876;
 Best Local Similarity 26.1%; Pred. No. 4.9; 40; Indels 42; Gaps 10;
 Matches 37; Conservative 23; Mismatches 40; Indels 42; Gaps 10;
 Ov 59 IWTINLICPCSRPMGIRASTGVFLGGGGYGLP-----PKERC---KIT 640
 Ov 66 INTI--RGFI--IREDIKEFLDIALMGSSTSINFSPYICBALPKPSFCRRKSGQIY 121
 Db 641 INLGDEBGGVNLBDVE---TAIRAKRC-----PICEFAMDAMIDDRK--LH 687
 Ov 122 YAGVNNPPE--FTIPOGQV 140
 Db 688 VCG--NNPNPCBGFTIVEEGEFKV 707

RESULT 9

CYSC_VIBPA STANDARD; PRT; 205 AA.
 ID CISC_VIBPA
 AC Q87S26;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Adenylyl sulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'-phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase).
 GN CYSC OR VP296.
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=2250854; PubMed=12820739;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Naito M., Shinano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shigematsu H., Hattori M., Iida T.;
 RA "Genome sequence of vibrio parahaemolyticus: a pathogenic mechanism

RT distinct from that of *V. cholerae*.
 CC Lancer 361:743-749(2003);
 CC Lancet 361:743-749(2003);
 CC -!- FUNCTION: Catalyzes the synthesis of activated sulfate.
 CC -!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
 CC phosphoadenylylsulfate.
 CC -!- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
 CC branch; second step.
 CC -!- SIMILARITY: Belongs to the APS kinase family.
 CC
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 CC
 CC EMBL; AP005073; BAC8559.1; -.
 DR HAMAP; MF_00065; -; 1.
 DR InterPro; IPR00891; APS kinase.
 DR Pfam; PF01583; APS kinase; 1.
 KW Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
 KW Phosphorylation; Complete proteome.
 NP BIND 39 46 ATP (BY SIMILARITY).
 FT ACT_SITE 113 113 PHOSPHOSERINE INTERMEDIATE (BY
 FT SIMILARITY).
 SQ SEQUENCE 205 AA; 22894 MW; 03689P141P4819F CRC64;
 Query Match 8.9%; Score 77; DB 1; Length 205;
 Best Local Similarity 26.3%; Pred. No. 1.1; Mismatches 50; Conservative 20; MisMatches 56; Indels 64; Gaps 14;
 Matches 50; Score 77; DB 1; Length 205;
 QY 2 KGFTATL-----FLWTLIFPSCSGGGGK-----AWPFWVCSDSGLVLYQ 43
 Db 21 KQFRALRKQKPAVLW--FTGIGLSGAGKSTVAGALENLRLAEGLGYHTLLDGN--VRHG 74
 QY 44 SCPLQDGFSVUKCKSKLNINRFG-----ILREDI-----KELFDIALLMSQGSV--LNF 97
 Db 75 LC---SDLGFS---EQRRENTR-RIGELAKUMADAGLIVLVSAPISPHRAEQLRD-- 124
 QY 87 LMSQGSSV--LNRSYPICEALPKFSFCGRKGE-----QIVKAGPVNPEFTIPOQ 136
 Db 125 LUEGEREFEVNAVASLEVCEGRUPKGKLKKARAGELENFTGIDSEVAPI-NPEIDLIPAG 183
 QY 137 EYQY---LISL 144
 Db 184 EKSVEELVEL 193
 RESULT 10
 CYSC_VIBVU STANDARD; PRT; 207 AA.
 ID CYSC_VIBVU STANDARD; PRT; 207 AA.
 AC 08DE75;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adenylyl-sulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-
 DE 5'-phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
 DE phosphotransferase).
 GN CRSC OR WI10723.
 OS Vibrio vulnificus.
 OC Bacterium; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 RN [1] NCBI_TAXID=672;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhoe J.-H.; Kim S.-Y., Chung S.-S., Kim J.-J., Moon Y.-H., Jeong H.,
 RA Choi H.-E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.;"
 RT Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
 RT -!- FUNCTION: Catalyzes the synthesis of activated sulfate.
 RT -!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
 CC
 CC -!- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
 CC branch; second step.
 CC -!- SIMILARITY: Belongs to the APS kinase family.
 CC
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 CC
 CC EMBL; AP016739; AAC09222.1; -.
 DR HAMAP; MF_00065; -; 1.
 DR InterPro; IPR00281; APS kinase.
 DR Pfam; PF01583; APS kinase; 1.
 DR ProDom; PD00350; APS kinase; 1.
 DR TIGR4Ms; TIGR0455; APK; 1.
 DR Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
 KW Phosphorylation; Complete proteome.
 NP BIND 39 46 ATP (BY SIMILARITY).
 FT ACT_SITE 113 113 PHOSPHOSERINE INTERMEDIATE (BY SIMILARITY).
 FT SIMILARITY).
 SQ SEQUENCE 207 AA; 22896 MW; 225B1A471139513 CRC64;
 Query Match 8.9%; Score 77; DB 1; Length 207;
 Best Local Similarity 25.0%; Pred. No. 1.1; Mismatches 45; Conservative 26; MisMatches 51; Indels 58; Gaps 13;
 Matches 50; Score 77; DB 1; Length 207;
 QY 10 LWTLIFPSSGG-----GGKWPTRVCSDSGLELYQOSCDPLQFGESTEK 57
 Db 35 LW--FTGIGLSGAGKSTVAGALENLRLAEGLGYHTLLDGN--VRHGLC--SDLGFS-- 82
 QY 58 CSKQKSNINRFG-----ILREDI-----KELFDIALLMSQGSV--LNF 97
 Db 83 -TQDERNTI-RIGELAKUMADAGLIVLVSAPISPHRAEQLRD--LIPPERGEIEVENT 138
 QY 98 SPICEDALPKFSFCGRKGEQIVYAG-----PVNNPEFTIPOQ--YQVILBLYTK 148
 Db 139 SLEVEQDRPKGLYKKARAGELENFTGIDSEVPL-NPEIDLIPAGEKSIALNDLVEQ 197
 RESULT 11
 VGLD_HSVEA STANDARD; PRT; 402 AA.
 ID VGLD_HSVEA STANDARD; PRT; 402 AA.
 AC P24672;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-APR-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycoprotein D precursor (Glycoprotein 17/18).
 OS GP OR GP17/18 OR 72.
 OS Equine herpesvirus type 1 (strain AB1) (EHV-1).
 OC Viruses; DNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=10328;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=92268892; PubMed=1316942;
 RX Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;
 RT "Identification of the equine herpesvirus type 1 glycoprotein 17/18
 RT as a homologue of herpes simplex virus glycoprotein D;"
 RL Gen. Virol. 73:1227-1233(1992).
 RN [2]
 RP SEQUENCE OF 242-402 FROM N.A.
 RX MEDLINE=9127627; PubMed=1647359;
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;
 RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
 RT herpesvirus type-1 short unique region;"
 RL Gene 101:203-208(1991).
 CC -!- SIMILARITY: Belongs to the herpesviruses glycoprotein D family.

CC -!- FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
 CC subunit on undecaprenyl-pyrophosphoryl-MurNAc-Pentaapeptide (lipid
 CC intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc-
 CC (Pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
 CC -!- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + MurNAc(Oyl-L-Ala-
 CC gamma-D-Glu-L-Tyr-D-Ala-D-Ala-diphosphoundecaprenol = UDP +
 CC GlcNAc-(1->4)-MurNAc(Oyl-L-Ala-D-Ala-D-Ala)-
 CC diphosphoundecaprenol.
 CC -!- PATHWAY: Peptidoglycan biosynthesis: last step.
 CC -- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
 CC -- SIMILARITY: Belongs to the glycosyltransferase family 28. Murg
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 CC
 DR EMBL; AL119077; CABY3295.1; .
 DR PIR; D81306.
 DR Rfam; MF_00033; -; 1.
 DR InterPro; IPR007235; Glyco_trans_2B.
 DR InterPro; IPR004276; Glyco_trans_2B.
 DR InterPro; IPR00509; Murg.
 DR Pfam; PF04101; Glyco_tran_2B_C; 1.
 DR TIGR4MS; TIGR013; mugI_1.
 DR KW Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane;
 KW Inner membrane; Peptidoglycan synthesis; Complete proteome.
 SQ SEQUENCE 342 AA; 38683 MW; F70131387068BB7 CRC64;

Query Match 8.8%; Score 75.5; DB 1; Length 342;
 Best Local Similarity 25.7%; Pred. No. 2; 8; Matches 37; Conservative 22; Mismatches 34; Indels 51; Gaps 11;

Db 35 DSGLEVIQSCDPLQDGFSVKSKQJKNINR----FQGILREBDKFLDLAAMS 89
 196 ENIKITHQ-CGK-NDF---BRCKKHQS-LNIQADIFPDSSINLKEKMN---ADAIISR 246

Oy 90 QSSVLSVFSYPSYCEAALP-----KF-----SFCCRKKCQIVYAGPVN 127
 247 AGASTL--FEGANTLPTIFFPYPAARKHNFQAFKFLQDQALC-----QIFMONSIN 297

Qy 128 NBFITIPOGEYVQVILELYTEKST 151
 298 LDEP-----FESILKLNLENIST 315

Db

RESULT 14

RPOB_CLOAB STANDARD; PRT; 1241 AA.

ID _RPOB_CLOAB AC 097EG9; DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (transcriptase
 beta chain) (RNA polymerase beta subunit).
 RN RPOB OR CAG3143.

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 Clostridium.

OX NCBI TaxId:1488;
 RN [1]

RP SEQUENCE FROM N_A.

RC STRAIN=ATCC 824 / DSM 792 / VRM B-1787;
 RX MEDLINE=2159325; PubMed=1466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RAatuson R.L., Sabath F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,

RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium aceto-butylicum.";
 RL J. Bacteriol. 183:4823-4838 (2001).

CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N). The enzyme consists of the sigma chain and the core
 CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
 CC beta' chain. Murg

CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.

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 CC
 DR EMBL; AL007809; ARX81081.1; .
 DR PIR; F97286; F97286.
 DR InterPro; IPR007120; RNA_pol_B.
 DR InterPro; IPR007624; RNA_pol_Rpb2_1.
 DR InterPro; IPR007622; RNA_pol_Rpb2_2.
 DR InterPro; IPR007615; RNA_pol_Rpb2_3.
 DR InterPro; IPR007120; RNA_pol_Rpb2_6.
 DR InterPro; IPR007610; RNA_pol_Rpb2_7.
 DR Pfam; PF04563; RNA_Pol_Rpb2_1.
 DR Pfam; PF04565; RNA_Pol_Rpb2_2.
 DR Pfam; PF04562; RNA_Pol_Rpb2_3.
 DR Pfam; PF04562; RNA_Pol_Rpb2_6.
 DR Pfam; PF04561; RNA_Pol_Rpb2_7.
 DR PROSITE; PS01166; RNA_Pol_BBTA_1.
 KW Transferase; Transcription; DNA-directed RNA polymerase;
 KW Complete proteome; RNA_Pol_BBTA_1.
 SQ SEQUENCE 1241 AA; 139248 MW; DEA50BA38EC4CB78 CRC64;

Query Match 8.8%; Score 75.5; DB 1; Length 1241;
 Best Local Similarity 19.3%; Pred. No. 14; Matches 29; Conservative 42; Mismatches 38; Indels 41; Gaps 9;

Db 35 DSGLEVIQSCDPLQDF-----GSVKEKSKQ---LKSINIRGI 73
 40 DNGLOEIPFDINPDIQYNTNLFLFIGYKLDMNIVKSYECKERDTYAAPLKVKRL 99

Qy 74 LRE--DIK--ELFL--DLAAMS--QGSSVLSVFSYPSYCEAALP----FSPCGRKQEIQY 122
 Db 100 NKETGEVKEQEVENGDPMLTGGTEFINGAERVIVSOLVRSRPGAYDYYVUNKGKLF 159

Qy 123 AGPVNNPEFTIPOGEYVQVILELYTEKSTV 152
 Db 160 ATVIPN-----RGAW---LEYEDTSNSV 180

RESULT 15

UAPI_HUMAN STANDARD; PRT; 522 AA.

ID _UAPI_HUMAN AC Q16222; DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE UDP-N-acetylxosamine pyrophosphorylase (Antigen X) (AGX) (Sperm-
 associated antigen 2) [Includes: UDP-N-acetylgalactosamine
 DE pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine
 DE pyrophosphorylase (EC 2.7.7.23) (AGX-2)].

GN UAPI OR SPAG2.

OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bivalvia; Bivalvia; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; NCBI_TaxID=9606; OS [1]

RP SEQUENCE FROM N.A. (ISOFORMS AGX1 AND AGX2).
 RC TISSUE=Testis;
 RX MEDLINE=94297079; PubMed=8025165;
 RA Diekman A.B.; Goldberg E.;
 RT "Characterization of a human antigen with sera from infertile
 RT patients."; Biol. Reprod. 50:1087-1093 (1994).
 RL [12]
 RN SEQUENCE FROM N.A. (ISOFORM AGX1).
 RP TISSUE=Testis;
 RX MEDLINE=98269105; PubMed=9603950;
 RA Mo T.; Yabe T.; Ariyama M.; Yamada-Okabe H.;
 RT "The eukaryotic UDP-N-acetylglucosamine Pyrophosphorylases: gene
 cloning, protein expression, and catalytic mechanism.";
 RL J. Biol. Chem. 273:14392-14397 (1998).
 RN [3]
 RP SOURCE FROM N.A. (AGX1/AGX2). PARTIAL SEQUENCE, AND
 RP CHARACTERIZATION.
 RC TISSUE=Breast cancer;
 RX MEDLINE=98038464; PubMed=9765219;
 RA Wang-Gillam A.; Pastuszak I.; Beilin A.D.;
 RT "A 17-amino acid insert changes UDP-N-acetylhexosamine
 RT Pyrophosphorylase specificity from UDP-GalNAc to UDP-GlcNAc."
 RL J. Biol. Chem. 273:27055-27057 (1998).
 CC -I- FUNCTION: AGX1 converts GalNAc-1-P into UDP-GalNAc in the presence
 of UTP. AGX2 catalyzes the synthesis of GlcNAc-1-P into UDP-GlcNAc
 in the presence of UTP.
 CC -I- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate
 CC = diphosphate + UDP-N-acetyl-D-glucosamine
 -I- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last) step.
 CC -I- SUBUNIT: Homodimer.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC. IN SPERMATOZOA, LOCALIZED TO
 THE PRINCIPAL PIECE OF THE TAIL, THE NECK REGION OF THE HEAD AND
 TO A LESSER EXTENT, THE MIDPIECE OF THE TAIL.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=AGX2; Synonyms=AGX-2;
 CC IsoId=01622-1; Sequence=Displayed;
 CC Name=AGX1; Synonyms=AGX-1;
 CC IsoId=Q16222; Sequence=VSP 004483;
 CC -I- TISSUE SPECIFICITY: Widely expressed. AGX1 is more abundant than AGX2 in somatic
 CC tissue than AGX2 while AGX2 is more abundant at low level in placenta, muscle and liver.
 CC -I- DISEASE: ANTIGEN IMPLICATED IN AUTOIMMUNE INFERTILITY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to licenses@isb-sib.ch).
 CC
 DR EMBL; S73498; AA331210; 2; -.
 DR AB011004; BR331202; 1; -.
 DR PDB; 1TV1; 28-AUG-02.
 DR PDB; 1TV3; 28-AUG-02.
 DR PDB; 1TVD; 29-AUG-02.
 DR PDB; 1TVG; 30-AUG-02.
 DR GeneW; HGNC:12457; UAP1.
 DR MIM; 603862; -.
 DR GO; GO:0003977; F:UDP-N-acetylglucosamine diphosphorylase act. . . ; TAS.
 DR GO; GO:005048; P:UDP-N-acetylglucosamine biosynthesis; TAS.
 DR InterPro; IPR026518; UDPGP.
 DR Pfam; PF011704; UDPGP; 1.
 KW Transferase; Nucleotidyltransferase; Antigen; Alternative splicing;
 KW Polymorphism; 3D-structure.
 SITE 111 111 BINDING SITE FOR HEXNAc-1-P
 FT (BY SIMILARITY).
 FT ACT-SITE 115 115 POTENTIAL.
 FT ACT-SITE 122 122 POTENTIAL.
 FT VARSPLIC 454 470 Missing (in isoform AGX1).
 FT /FTId=VSP_004483.

| FT | VARIANT | 418 | 418 | P -> H (in dbsnp:1128539).
/FTId=VAR_014935. |
|-----------------------|----------|-------------------------------------------------------------|----------------|-------------------------------------------------|
| FT | CONFLICT | 454 | 454 | MISSING (IN REF. 1). |
| FT | SEQUENCE | 522 AA; | 58840 MW; | C823A9AD8659A135 CRC64; |
| SQ | | | | |
| Query Match | | 8.7% | Score 75; | DB 1; Length 522; |
| Best Local Similarity | | 23.7% | Pred. No. 5,4; | Gaps 6; |
| Matches | | 28; | Mismatches 35; | Indels 36; |
| Conservative | | 19; | | |
| QY | 27 | WPTHWVCSDSLGVLYQSODPLODFGSVKE--CSKQL--KSNINIRGIIRED-- | 77 | |
| Db | 245 | WSTHRYCVNND--ILVKVADP-RFIGCICOKGKadCGAKVWEKNPTEPVGWCVRGIVYQ | 300 | |
| OY | 78 | -IKELFLDIALMSQGSVNVFSYSPICEAALPKFSCFCRRKGSEQIYVAGPVANPEFTIP | 134 | |
| Db | 301 | WVEYSEISIAATAQKRS-----dGRLLFNAGNTIANHFTWP | 336 | |

Search completed: April 29, 2004, 15:24:51
 Job time : 18 secs

Possible occludin/ELL family.

RESULT 2
 ID 082196 PRELIMINARY; PRT; 1137 AA.
 AC 082196;
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
 DE Copi-like retroelement pol polyprotein.
 GN AT2G19840
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Spermatophyta; Viridiplantae; Streptophyta; Tracheophyta;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=cvv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnsteed M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.E., Roering C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.J., Umeyam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrer A.J., Cleasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhagen G.P., Preiss D., Nieman W.C., White O., Eisen J.A.,
 RA Salberg S.L., Fraser C.M., Vertter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*
 RT *thaliana*." *Nature* 402:761-768(1999).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cvv. Columbia;
 RA Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC005169; AAC62132.1; -.
 DR PIR; G84581; G84581.
 DR GO; GO-003677; F:DNA binding; IEA.
 DR GO; GO-000610; 2' DNA recombination; IEA.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR01878; Znf_CCHC.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00038; Zf-CCHC; 1.
 DR PRINTS; PR00939; C2HC_C2HC_PINGER.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS50158; ZF_CCHC; 1.
 DR Polyprotein.
 SQ SEQUENCE 1137 AA; 129775 MW; 7265DP09C6E1025C CRC64;
 Query Match 11.5%; Score 99; DB 10; Length 1137;
 Best Local Similarity 26.3%; Pred. No. 0.15; Mismatches 42; Indels 36; Gaps 7;
 Matches 36; Conservative 23; Mismatches 42; Indels 36; Gaps 7;

RESULT 4
 ID Q9LV30 PRELIMINARY; PRT; 1440 AA.
 AC Q9LV30;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Emb CAB40755.1.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=0361099; PubMed=10307853;
 RA Nakamura Y.;
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety PI, TAC and BAC clones";
 RT DNA Res. 7:217-221(2000).
 DR EMBL; AB020749; BAB2023.1; -.
 DR InterPro; IPR02885; PPR.
 DR InterPro; IPR008941; TPR-like.
 DR Pfam; PF01535; PPR; 25.
 DR TIGRFAM; TIGR0756; PPR; 24.
 SQ SEQUENCE 1440 AA; 162336 MW; 364887F23B8B9BP CRC64;
 Query Match 9.6%; Score 83; DB 10; Length 1440;

Best Local Similarity 22.5%; Pred. No. 11; Mismatches 57; Indels 14; Gaps 3; Matches 27; Conservative 22; Mismatches 57; Indels 14; Gaps 3;

QY 30 HWCVSQSGLETVYQSCDPLQDFGFVVEKCKQQLKNINTRFGTILREDIKEFLDLMAS 89
Db 830 HALCVDRGLBLLVVYVVEBQDMGFKLSSTILMUDAFARAGNF--EVKVISSMKAG 897
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cvv. Columbia;
RX MEDLINE=20033487; PubMed=10617197;
RA Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.I., Mason T.M., Bowman C.L., Barnstead M.F., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Kao H., Moifat K.S.,
RA Cronin D.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Freyss D., Nieman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007071; ARD24845.1; --.
DR PIR; HB1723; HB4223.
DR GO; GO:000324; P: catalytic activity; IEA.
DR GO; GO:004806; P: triacylglycerol lipase activity; IEA.
DR GO; GO:006629; P: lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase 3.
DR InterPro; IPR000379; Ser_endTS.
DR PIR; PP0176; Lipase 3; 1.
SQ SEQUENCE 484 AA; 54923 MW; 74650CD21BB783D3 CRC64;

Query Match 9.2%; Score 79.5%; DB 10; Length 484;
Matches 34; Conservative 27.4%; Pred. No. 6, 8; Mismatches 43; Indels 29; Gaps 5;

RT Thermophilic archaeabacterium, Pyrococcus horikoshii OT3.;
RL DNA Res. 5:55-75 (1998).
DR EMBL; AP000002; BAA2405.1; -.
DR PIR; H71139; H71139.
DR InterPro; IPR02881; DUF58.
DR Pfam; PF01682; DUF58; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 45912 MW; 69485F5337C5DD8D CRC64;

Best Local Similarity 9.4%; Score 81; DB 17; Length 406;
Matches 39; Conservative 27; Mismatches 49; Indels 36; Gaps 9;

QY 1 MGKG-FPATLFWTLIPFSCSGGGGKA-WPMPHVCSDSGLVEVYQSCDPLQDFGP--SV 55
Db 4 MKGASFFVTFLFWMFIVMSLIFGVPGKLAUFPILLI--MGILF--DARGDFVEREI 56
RN [1]
QY 56 EKC---SKQKSGNINTRFG---ILLRDEKELFLDLMASQGSQSVLFSYPICEAL 106
Db 57 EKQQTFWNEIEVLRVVRVGIGLVAENPKAF---MTSSGSNVGF----- 103
QY 107 PRPSFCGRKGQIYVAGPVNNEPTIPQGE 137
Db 104 --PTYGRRSFQSLSYKULPKRGVYEIPKE 132
RESULT 6
Q9SING9 PRELIMINARY; PRT; 484 AA.
ID Q9SING9
AC Q9SING9;
DT 01-MAY-2000 (TREMBrel. 13, Created)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE putative triacylglycerol lipase.
OS Arvadg31690.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;
OC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosididae II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBITAXID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cvv. Columbia;
RX MEDLINE=20033487; PubMed=10617197;
RA Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.I., Mason T.M., Bowman C.L., Barnstead M.F., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Kao H., Moifat K.S.,
RA Cronin D.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Freyss D., Nieman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007071; ARD24845.1; --.
DR PIR; HB1723; HB4223.
DR GO; GO:000324; P: catalytic activity; IEA.
DR GO; GO:004806; P: triacylglycerol lipase activity; IEA.
DR GO; GO:006629; P: lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase 3.
DR InterPro; IPR000379; Ser_endTS.
DR PIR; PP0176; Lipase 3; 1.
SQ SEQUENCE 484 AA; 54923 MW; 74650CD21BB783D3 CRC64;

Query Match 9.2%; Score 79.5%; DB 10; Length 484;
Matches 34; Conservative 27.4%; Pred. No. 6, 8; Mismatches 43; Indels 29; Gaps 5;

RT Thermophilic archaeabacterium, Pyrococcus horikoshii OT3.;
RL DNA Res. 5:55-75 (1998).
DR EMBL; AP000002; BAA2405.1; -.
DR PIR; H71139; H71139.
DR InterPro; IPR02881; DUF58.
DR Pfam; PF01682; DUF58; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 406 AA; 45912 MW; 69485F5337C5DD8D CRC64;

Best Local Similarity 9.4%; Score 81; DB 17; Length 406;
Matches 39; Conservative 27; Mismatches 49; Indels 36; Gaps 9;

QY 1 MGKG-FPATLFWTLIPFSCSGGGGKA-WPMPHVCSDSGLVEVYQSCDPLQDFGP--SV 55
Db 4 MKGASFFVTFLFWMFIVMSLIFGVPGKLAUFPILLI--MGILF--DARGDFVEREI 56
RN [1]
QY 56 EKC---SKQKSGNINTRFG---ILLRDEKELFLDLMASQGSQSVLFSYPICEAL 106
Db 57 EKQQTFWNEIEVLRVVRVGIGLVAENPKAF---MTSSGSNVGF----- 103
QY 107 PRPSFCGRKGQIYVAGPVNNEPTIPQGE 137
Db 104 --PTYGRRSFQSLSYKULPKRGVYEIPKE 132
RESULT 7
Q9VSU2 PRELIMINARY; PRT; 2786 AA.
ID Q9VSU2
AC Q9VSU2
DT 01-MAY-2000 (TREMBrel. 13, Created)
DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
DE CG4821 protein.
OS Drosophila melanogaster (Fruit fly).
OC Drosophila melanogaster (Fruit fly).
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriodea; Drosophilidae; Drosophila.
OC NCBITAXID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celmer S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaraides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandt R.C., Rogers Y.H.C., Blazej R.G., Champine M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Borkova D., Bortchan M.R., Bouck J., Brokstein P., Brottier P., Bolshakov S.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delchev A., Deng Z.,
 RA Dodson K., Douc T.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabreliam A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey J., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moarry C., Morris J., Moskrafi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nixon K.A., Nixon K., Nussbaum D.R., Pacie J.M.,
 RA Palazzolo M., Pittman G.S., Pani S., Pollard J., Purif V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Stiang R., Sun S.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Benson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Chamee M., Daveyport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresner D., Farran D.,
 RA Ferrera E., Frise E., Gallo R., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Howland T.J.,
 RA Inegwam C., Jalali M., Kruse D., Li P., Mattel B., Moskrafi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nelson J.,
 RA Paclib J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Prokunina-Long S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Slepchenko M., Strong R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of *Drosophila melanogaster* genome";
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Terry J.L., Bergman C., Berman C., Carlson J.W., Celinker S.E., Smith C.D.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smrutiak P., Whittlefield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
 DR EMBL; AE003553; AF050319; 3; -
 DR HSSP; P00750; IRTF
 DR FlyBase; FBgn0023479; Tequila.
 GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0008961; F:chitin binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008213; F:peptidase activity; IEA.
 DR GO; GO:000504; F:scavenger receptor activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:006030; F:chitin metabolism; IEA.
 DR GO; GO:006508; F:protein transport; IEA.
 DR GO; GO:0015932; F:proton transport; IEA.
 DR InterPro; IPR00194; ATPase_alpha/beta.
 DR InterPro; IPR020257; Chitin_bind_Per1.
 DR InterPro; IPR00903; Cys_Ser_trypsin.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR00154; Peptidase_SI.
 DR InterPro; IPR001314; Peptidase_SIA.
 DR InterPro; IPR001190; Ssrp_receptor.
 DR Pfam; PRO01607; CRM_14; 15.
 DR Pfam; PRO0057; Idin_recept_a; 2.
 DR Pfam; PRO00530; SRP_R; 2.
 DR Pfam; PRO0089; trypsin_1.
 DR PRINTS; PRO0122; CHYMOTRYPSIN.
 DR PRINTS; PRO0261; DILRECEPTOR.
 DR PRINTS; PRO0258; SPERACTRCPR.
 DR SMART; SM00494; CHCBDD2; 15.
 DR SMART; SM00192; LDIRA_2; 2.
 DR SMART; SM00202; SR; 2.
 DR SMART; SM00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 2786 AA; 308362 MW; 2EEB7A7D5002C76 CRC64;
 DR Query Match 9.2%; Score 79; DB 5; Length 2786;
 DR Best Local Similarity 26.9%; Pred. No. 63; Mismatches 36; Indels 20; Gaps 6;
 DR Matches 28; Conservative 20; Mismatches 36; Indels 20; Gaps 6;
 Qy 12 TLIFPSCSGGGG-KAWP---TIVWCDSGLVYQSCDPLQDFGSVVKC---SKWIK 64
 Db 770 TWIISACPDTCNGHLHYPIPDAGKTVRCSDGG-KMSIQECCNQMAFSQSQRCPRLIST 828
 Qy 65 NINIRGIGLIREDI-----KELFLDIALMSQGSVSVNFSPV 100
 Db 829 EDVRVP---REELQIQTWYSSODIOQOOSPLKBCPSVLRGNYP 868

RC STRAIN=AB972;
 RA Badcock K.; Churcher C.M.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB972;
 RA Barrell B.; Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z71255; CAB95018.1; -.
 DR EMBL; Z49244; CAB89216.1; -.
 DR PIR; S54495; S54496.
 DR PROSITE; PS00028; Zinc_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; Zinc_FINGER_C2H2_2; 2.
 KW Hypothetical protein; Metal-binding; Zinc-finger.
 SQ SEQUENCE 1133 AA; 130116 MW; 77663C9E3760DAA CRC64;
 Query Match 9.0%; Score 78; DB 3; Length 1133;
 Best Local Similarity 25.3%; Pred. No. 27; Indels 31; Gaps 8;
 Matches 37; Conservative 16; Mismatches 62;
 DR PIR0096; zf-C2H2_2.
 DR SMART; SMO035; Znf_C2H2_1.
 DR PROSITE; PS00028; Zinc_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; Zinc_FINGER_C2H2_2; 2.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2_2.
 DR SMART; SMO035; Znf_C2H2_1.
 DR PROSITE; PS00028; Zinc_FINGER_C2H2_1; 1.
 DR PROSITE; PS0157; Zinc_FINGER_C2H2_2; 2.
 DR InterPro; IPR00114; Peptidase_S1.
 DR InterPro; IPR001190; Srcr_receptor.
 DR Pfam; PF01607; CBM_14; 10.
 DR Pfam; PF00057; IgL_recept_a; 2.
 DR Pfam; PF00530; SRCR_2.
 DR Pfam; PF0088; trypsin; 1.
 DR PRINTS; PR00722; CHYMORYPIN.
 DR PRINTS; PR00261; IDLRECEPTOR.
 DR PRINTS; PR00258; SPERACTRCPR.
 DR SMART; SMO0494; ChtbD2; 10.
 DR SMART; SMO0192; India_2.
 DR SMART; SN00202; SR_2.
 DR SMART; SN00200; TRYF_SPEC_1.
 DR PROSITE; PS00152; ATPase_alpha_beta; 1..
 DR PROSITE; PS01209; LDRA_1; 1.
 DR PROSITE; PS0066; LDRA_2; 2.
 DR PROSITE; PS00420; SRCR_1; 2.
 DR PROSITE; PS50287; SRCR_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SBR; 1.
 DR HYDROLASE; Protease; Serine protease.
 SQ SEQUENCE 2409 AA; 267618 MW; 4F014411D0B87150 CRC64;
 Query Match 9.0%; Score 78; DB 5; Length 2409;
 Best Local Similarity 25.0%; Pred. No. 68; Indels 36; Gaps 6;
 Matches 27; Conservative 21; Mismatches 36;
 DR Q9YU77 PRELIMINARY; PRT; 2409 AA.
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-OCT-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE SP0286P.
 GN Q9YU77
 OS Drosophila OR CG4821 OR CG4948 OR CG18403.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuncio J., Paclib J., Paraga V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celisier S.,
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR HSPB; P00751; LAN1.
 DR FBG002479; Tequila.
 DR GO; GO:0005576; C: extracellular; IEA.
 DR GO; GO:0015020; C:membrane; IEA.
 DR GO; GO:0005524; FAMP binding; IEA.
 DR GO; GO:0008001; F-chitin binding; IEA.
 DR GO; GO:0004233; F-chymotrypsin activity; IBA.
 DR GO; GO:000823; F-peptidase activity; IBA.
 DR GO; GO:000504; F-scavenger receptor activity; IBA.
 DR GO; GO:0004225; F-tryptipin activity; IBA.
 DR GO; GO:0006030; F-chitin metabolism; IBA.
 DR GO; GO:0006506; F-proteolysis and peptidolysis; IBA.

DR GO; GO:0015992; P:proton transport; IBA.
 DR InterPro; IPR001194; ATPase_a/bcentre.
 DR InterPro; IPR002357; Chitin-bind_Pera.
 DR InterPro; IPR009003; CyS_Ser_trypsin.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR001554; Peptidase_S1.
 DR InterPro; IPR00114; Peptidase_S1A.
 DR InterPro; IPR001190; Srcr_receptor.
 DR Pfam; PF01607; CBM_14; 10.
 DR Pfam; PF00057; IgL_recept_a; 2.
 DR Pfam; PF00530; SRCR_2.
 DR Pfam; PF0088; trypsin; 1.
 DR PRINTS; PR00722; CHYMORYPIN.
 DR PRINTS; PR00261; IDLRECEPTOR.
 DR PROSITE; PS0066; LDRA_2; 2.
 DR PROSITE; PS00420; SRCR_1; 2.
 DR PROSITE; PS50287; SRCR_2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SBR; 1.
 DR HYDROLASE; Protease; Serine protease.
 SQ SEQUENCE 394 AA; 44831 MW; 3929C66B1A95245 CRC64;
 Query Match 9.0%; Score 77.5; DB 17; Length 394;
 Best Local Similarity 23.4%; Pred. No. 8.7; Indels 44; Gaps 9; Mismatches 36; Conservative 31; Mismatches 44; Indels 43; Gaps 9;

QY 1 MKG--FTATIFLWTIILPPCSGGGGKA_WPTHVVCSDSLQDPLQDFGSVER 57
 Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Yersinia.
 OC
 OC
 NCBI_Taxid=32;

Db 58 -----CSKOLKSNIINRFG---TREDIKEFLDIALMSQSSVNL_FSYPICE 103
 SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biorar Orientalis;
 RX MEDLINE=1470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sabatti C., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies M.J., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jade S., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stansfield K., Whitehead S., Barrell B.G.;
 RT "Genome Sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:521-527(2001).
 DR EMBL: AJ41456; CA92476.1; -.
 DR PIR: AH033; AH0393;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 246 AA; 27994 MW; 83PFA145C2F82BC CRC64;

QY 01-JAN-1998 (TREMBREL_05, Created)
 DT 01-OCT-2003 (TREMBREL_25, Last annotation update)

DE S glycoprotein (Fragment)
 OS Brassica oleracea (Cauliflower).
 OC Spematophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;

RN [1].

RP SEQUENCE FROM N.A.
 RX MEDLINE=9735258; PubMed=9207151;
 RA Kubota M., Nishio T., Satta Y., Hinata K., Okendan D.;
 RT "Striking sequence similarity in inter- and intra-specific comparisons
 o f class I Sig alleles from *Brassica oleracea* and *Brassica*
 campenstris: Implications for the evolution and recognition
 mechanism"; Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
 RT PROC. NATL. ACAD. SCI. U.S.A. 94:7673-7678(1997).
 RL EMBL: DB5205; BAA21939.1; -.

DR PIR: TA4529; "TA4529."
 DR GO:0005520; P:sugar binding; IEA.
 DR InterPro: IPR01480; B_lectin.
 DR InterPro: IPR03609; Pan_app.
 DR InterPro: IPR00858; Slclocus_glycop.

DR Pfam: PF01453; Agglutinin; 1.
 DR SMART: SM00954; S1 locus glycop; 1.
 DR SMART; SM00103; B_lectin; 1.
 DR SMART; SM00473; PAN_AP; 1.
 FT NON_TER 428 428
 FT SEQUENCE 426 AA; 48724 MW; 18E04542C7293BEA CRC64;

QY 9 0%; Score 77.5; DB 10; Length 428;
 Best Local Similarity 25.2%; Pred. No. 9.7; Indels 27; Mismatches 20; Gaps 4; Matches 49; Conservatve 49; Index 11; Gaps 4;

Db 49 QDPGEVSEVKQQLKSNIINRFG---TREDIKEFLDIALMSQSSVNL_FSYPICE 108
 DR Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF072549; AAC27549.1; -.
 DR InterPro: IPR007226; SAG.
 DR Pfam: PF0092; SAG; 1.
 DR PRINTS: PRO1801; SURFACEANTIGN.
 SQ SEQUENCE 396 AA; SUR42105 MW; 7E96A39P44D15A02 CRC64;

QY 8.9%; Score 77; DB 5; Length 396;
 Best Local Similarity 21.1%; Pred. No. 10; Indels 54; Gaps 6; Mismatches 37; Conservatve 22; Gaps 6; Matches 37;

Db 24 GGMPPHTVCCSDGL--EVLYQSCDPLQDFPSVAKCSKQLKSNIINR----- 69
 DR 170 GMMWTLQLESPSLPLDKKAFPGCDNFKAGAKDVKQVSKECKDENTKRSVAENVV 229

QY 70 -----FGTIRREDIKEFLDIALMSQSSVNL_FSYPICE 99
 DR 230 TCAGKESNPPLNVEMTMLTIOCGSISGVINPNSYAFCDL---QDTDMQTC 285

GN Putative exported protein.
 GN YPO3241.

OS Yersinia pestis

RESULT 12

Q8ZBY9 PRELIMINARY; PRT; 246 AA.
 ID Q8ZBY9 . PRELIMINARY; PRT; 246 AA.
 AC Q8ZBY9 . PRELIMINARY; PRT; 246 AA.
 DT 01-MAR-2002 (TREMBREL_20, Created)
 DT 01-MAR-2002 (TREMBREL_20, Last sequence update)
 DT 01-JUN-2003 (TREMBREL_24, Last annotation update)
 DR Putative exported protein.

DR PR; G96740; G96740; 84156 MW; 9EDASEERF88BAEB CRC64;
 SQ SEQUENCE 739 AA; 84156 MW; 9EDASEERF88BAEB CRC64;
 Query Match 8.9%; Score 77; DB 10; Length 739;
 Best Local Similarity 24.0%; Pred. No. 21;
 Matches 25; Conservative 17; Mismatches 30; Indels 32; Gaps 4;
 DR 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Nicotinic acetylcholine receptor beta 1b subunit (Fragment).
 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TAXID=3103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jones A.K.; Elgar G.; Sattelle D.B.;
 RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
 Pugn rubripes.",
 RL Genomics 010-01(2003);
 DR EMBL: AY299468; AAPR88383.1; -.
 KW Receptor.
 PT NON TER 1 1
 SQ SEQUENCE 480 AA; 55233 MW; D0CD2322938E05C0 CRC64;
 Query Match 8.9%; Score 77; DB 13; Length 480;
 Best Local Similarity 29.9%; Pred. No. 13;
 Matches 23; Conservative 14; Mismatches 24; Indels 16; Gaps 4;
 RT Pugn rubripes.
 OX 23 GSKAW PTHVUVSVDGKLVYSCDPLQDFGGSVEKSKQLKS-----NTNIRGIGILR 75
 DB 115 GRVWTWPALYSSCGVKVEY-----FPFDWQNCSMQRSSYIVDSTDIDVQYALNR 166
 OX 76 -DIKEFLFLDILMSQG 91
 DR 167 GDBIREIOLDEAFTEGG 183

RESULT 15

O9M9G4 PRELIMINARY; PRT; 739 AA.
 ID O9M9G4
 AC O9M9G4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-JUN-2003 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE FL4O23_20 protein.
 GN FL4O23_20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. columba;
 RA Liu S., Yu G., Lee J., Sakano H., Jhaveri A., Lenz C., Toriumi M.,
 RA Chin C., Choi J., Choi E., Gonzalez A., Howng B., Koo T., Li J., Conn L.,
 RA Liu A., Pham P., Vaysseberg M., Altafi H., Buehler R., Chao Q., Conn L.,
 RA Conway A.B., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Nguyen M., Palm C., Shinn P., Tambungga G., Davis R., Ecker J.,
 RA Federspiel N., Theologis A.;
 RT "The sequence of BAC FL4O23 from Arabidopsis thaliana chromosome 1.,";
 RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. columba;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC012654; AAF43255.1; -.